(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification[7]: G01N 33/68, 33/574

(21) International Application Number:
PCT/EP2003/014057

(22) International Filing Date:
11 December 2003 (11.12.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
02028058.2   17 December 2002 (17.12.2002)   EP
03025237.3   5 November 2003 (05.11.2003)   EP

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(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: SPECIFIC MARKERS FOR PANCREATIC CANCER

(57) Abstract: The present invention provides polypeptides which are up- or down-regulated in pancreatic cancer and which can be used as markers for diagnosis of pancreatic cancer. The invention also provides an in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of a) obtaining a biological sample; and b) detecting and/or measuring the increase of one or more polypeptides as disclosed herein. Furthermore, screening methods relating to inhibitors and antagonists of the specific polypeptides disclosed herein are provided.

Specific Markers for Pancreatic Cancer

The present invention relates to markers for diagnosis of pancreatic cancer comprising at least one polypeptide identified by proteomics to be up-regulated in pancreatic cancer, to an in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of a) obtaining a biological
5   sample; and b) detecting and/or measuring the increase of specific markers as disclosed herein. Furthermore, screening methods relating to antagonists of the specific markers disclosed herein are provided.

10   Pancreatic cancer is a common cause of death in the Western world. It is one of the most aggressive malignant tumors, with an overall 5-year survival rate of 0.4%. In many patients with pancreatic cancer, accurate preoperative diagnosis is difficult to achieve with conventional imaging analyses. Most patients with pancreatic cancer present late in the course of the disease and have either locally extensive or metastatic disease. Overall,
15   only up to 20% are candidates for resection and have the potential for curative surgery. Among the causes for this late presentation is the lack of diagnostic methods for an earlier detection of the disease. Besides this lack of diagnostic methods, the high mortality of patients with pancreatic cancer is additionally caused by a lack of effective treatments. Therefore, the identification of new targets for early diagnosis of pancreatic tumors, and
20   for the development of agents to treat pancreatic cancer is a challenge of paramount importance.

The problem of identifying polypeptides suitable as markers of pancreatic cancer
25   for early diagnosis of the disease, and the long felt need for such markers, was overcome by the present invention by applying the new technology of proteomics. It was surprisingly found by using proteomic technology that a specific set of polypeptides are differentially expressed in pancreatic tissue obtained from individuals suffering from HR/03.11.2003

pancreatic cancer, as compared to healthy pancreatic tissue. Said differentially expressed polypeptides are listed in appended tables 2 and 3. The polypeptides in table 3 are encoded by genes which were previously identified to be up-regulated in pancreatic cancer on the transcriptional level (Iacobuzio-Donahue et al., (2002), Am. J. Pathol. 160,

5   1239-1249). However, it is well known that regulation on the transcriptional level is not necessarily indicative of a similar regulation of the expression of the respective gene on the translational level. Thus, only by demonstrating that the polypeptides listed in table 3 are up-regulated in pancreatic cancer is it possible to use them for polypeptide-based diagnostic assays for the detection of pancreatic cancer.

10

Based on the polypeptides listed in tables 2 and 3, the present invention provides a marker for diagnosis of pancreatic cancer comprising at least one polypeptide selected from the group consisting of the polypeptides listed in tables 2 and/or 3 (Seq ID No. 1 to 24 and 26 to 49; and/or Seq ID No. 25 and 50 to 55). Thus, the term "marker" as used

15   herein refers to one or more polypeptides that are regulated in cancer and that can be used to diagnose pancreatic cancer or a susceptibility to pancreatic cancer either alone or as combinations of multiple polypeptides that are known to be regulated in pancreatic cancer. Preferably, said polypeptides are selected from the group consisting of Seq. ID No. 2 to 10, 12 to 15, 17, 19, 20, 23, 24, 27, 28, 31 to 40, 42 to 45, 47 and 48; and/or Seq

20   ID No. 25 and 50 to 54. More preferably, said polypeptides are selected from the group consisting of Seq ID No. 3, 4, 6, 9, 14, 15, 27, 31 to 35, 37, 39, 40; and/or Seq ID No. 50 to 52. Even more preferably, said polypeptides are selected from the group consisting of Seq ID No. 4, 6, 9, 14, 15, 31, 33 to 35 and/or Seq ID No. 51 and 52. Most preferably, said polypeptides are selected from the group consisting of Seq ID No. 4, 6, 14, 15 and 31;

25   and/or Seq ID No. 52.

The term "polypeptide" as used herein, refers to a polymer of amino acids, and not to a specific length. Thus, peptides, oligopeptides and proteins are included within the definition of polypeptide.

30

Preferably, the marker of this invention is a marker comprising at least one polypeptide selected from the group consisting of the polypeptides listed in table 2.

Furthermore, a polypeptide selected from the group consisting of the polypeptides listed in tables 2 and/or 3, is used as a marker or as part of a marker for diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer. Preferably, said

5   polypeptides are selected from the group consisting of Seq. ID No. 2 to 10, 12 to 15, 17, 19, 20, 23, 24, 27, 28, 31 to 40, 42 to 45, 47 and 48 from table 2 and/or Seq ID No. 25 and 50 to 54 from table 3. These polypeptides are induced at least two fold, as can be seen in tables 2 and 3. More preferably, said polypeptides are selected from the group consisting of Seq ID No. 3, 4, 6, 9, 14, 15, 27, 31 to 35, 37, 39, 40 from table 2 and/or Seq ID No. 50

10   to 52 from table 3. These polypeptides are induced at least three fold, as can be seen in tables 2 and 3. Even more preferably, said polypeptides are selected from the group consisting of Seq ID No. 4, 6, 9, 14, 15, 31, 33 to 35 from table 2 and/or Seq ID No. 51 and 52 from table 3. These polypeptides are induced at least 4 fold, as can be seen in tables 2 and 3. Most preferably, said polypeptides are selected from the group consisting

15   of Seq ID No. 4, 6, 14, 15 and 31 from table 2 and/or Seq ID No. 52 from table 3, which are the polypeptides that are induced five fold, as shown in tables 2 and 3.

The present invention pertains to a marker for diagnosis of pancreatic cancer comprising at least one polypeptide selected from the group consisting of the

20   polypeptides listed in table 6. Preferably, said at least one polypeptide additionally does not include Seq ID No.s 25 and 50 to 55.

In a preferred embodiment, the marker hereinbefore described additionally comprises at least one of the polypeptides listed in table 5.

25

Several groups of polypeptides were identified as markers for pancreatic cancers:

Enzymes

One of the enzymes that caught our attention was Glutamine γ-glutamyltransferase/tissue transglutaminase (TGLC, Seq ID No. 54). It is a member of the

30   transglutaminase family that catalyzes Ca2+ dependent reactions resulting in the post translational modification (cross-linking and conjugation with polyamines) of proteins at

the level of glutamine and lysine residues (Greenberg, C. S., Birckbichler, P. J., and Rice, R. H. Transglutaminases: multifunctional cross-linking enzymes that stabilize tissues. FASEB J., *5*: 3071-3077, 1991). Many different roles for this protein have been described, among them apoptosis, adhesion, and differentiation (Amendola, A., Fesus, L.,

5 Piacentini, M., and Szondy, Z. "Tissue" transglutaminase in AIDS. J.Immunol.Methods, *265*: 145-159, 2002). There is some controversy on the role of TGLC in apoptosis. While several pieces of evidence suggest that TGLC is a pro-apoptotic protein (Melino, G., et al., Mol.Cell Biol., *14*: 6584-6596, 1994), Jason et al. found that TGLC acts in anti-apoptotic fashion (Boehm, J. E., et al. J.Biol.Chem., *277*: 20127-20130, 2002). Many substrates of

10 TGLC are major extra-cellular matrix (ECM) components such as fibronectin, osteonectin, and collagen, which makes TGLC an important enzyme in ECM development (Raghunath, M., et al., J.Clin.Invest, *98*: 1174-1184, 1996., Nemes, Z., Jr., et al. J.Biol.Chem., *272*: 20577-20583, 1997). Abnormal ECM development is involved in many pathological conditions such as fibrosis and may play a role in the proliferation of

15 fibrous tissue observed in PC. Haroon et al. described that TGLC ECM-promoting abilities are an important part of the host response mechanism against tumor growth (Haroon, Z. A., et al., Lab Invest, *79*: 1679-1686, 1999). Interestingly, loss of TGLC can be a biomarker for prostate adenocarcinoma (Birckbichler, P. J., et al., Cancer, *89*: 412-423, 2000), which raises the question whether the measured TGLC is produced by neoplastic

20 ductal cells and/or stromal cells. Measurements of mRNA levels in PC, normal tissue and PC cell lines indicate that TGLC is over expressed in both cell types (Iacobuzio-Donahue, C. A., et al., Am.J.Pathol., *160*: 1239-1249, 2002), which would distinguish PC from prostate adenocarcinoma.. Therefore, one preferred embodiment of the present invention is a marker comprising Seq ID No. 54.

25 Cytoskeletal proteins

Several cytoskeletal proteins were detected at higher levels in PC than in surrounding tissue. One of these is gelsolin (Seq ID No. 3), a Ca^{2+} and PIP2 (polyphosphoinositide 4,5-bisphosphate) regulated severing and capping protein, which is a multifunctional actin regulatory protein and has roles in actin remodeling, motility,

30 signaling, apoptosis and cancer (Maruta, H. G proteins cytoskeleton and cancer.Austin, Tex.: R.G. Landes, 1998). In several cancer studies, gelsolin expression has been described as down-regulated during carcinogenesis (breast, colon, stomach, bladder, prostate, and lung) (Asch, H. L., et al., Cancer Res., *56*: 4841-4845, 1996; Dosaka-Akita, H., et al., Cancer Res., *58*: 322-327, 1998, Prasad, S. C., et al. Electrophoresis, *18*: 629-637, 1997).

35 Another example for an up-regulated cytoskeletal protein is fascin (Seq ID No. 58), an

- 5 -

actin-bundling protein that has a role in cell matrix adhesion, cell interaction and
migration. Fascin over expression has been reported in several cancers, such as breast,
colon, and ovarian carcinoma (29). The present invention also features fascin 2 as a
polypeptide up-regulated in pancreatic cancer (Seq ID No. 56). Thus, a preferred
5   embodiment of the present invention is a marker comprising Seq ID. No. 3. In another
preferred embodiment, the marker comprises Seq. ID No. 58. In another preferred
embodiment, the marker comprises Seq. ID No. 56.

In our study, cytokeratin 7 (Seq. ID No. 52) and cytokeratin 19 (Seq ID No. 33)
showed strong expression in PC. Both have also been described in other cancers and have
10   been linked with metastasis formation (Moll, R., Int.J.Biol.Markers, 9: 63-69, 1994.).
High protein levels of actinin-4 (Seq ID No. 5) were detected in PC. This protein was
linked by others with cell motility and cancer invasion (Honda, K., Yamada, T., Endo, R.,
Ino, Y., Gotoh, M., Tsuda, H., Yamada, Y., Chiba, H., and Hirohashi, S. J.Cell Biol., 140:
1383-1393, 1998.). Taken together, the apparent strong expression of cytoskeletal
15   proteins is likely to be an important factor in the strong invasiveness and metastasis-
forming potential of PC. Thus, a preferred embodiment of the present invention is a
marker comprising Seq ID. No. 52. In another preferred embodiment, the marker
comprises Seq. ID No. 33. In another preferred embodiment, the marker comprises Seq.
ID No. 5.

20   Metastasis

Cancer of exocrine pancreas is characterized by extensive local invasion, early
lymphatic and hematogenous metastasis. Metastasis in PC has been found in the
skeleton, eye, bladder, etc. The extent of angiogenesis depends on the balance between
pro-angiogenic or anti-angiogenic factors released from cancer and host cell. Currently,
25   intratumoral microvessel density (IMD) measured by immunocytochemistry appears to
be the most reliable parameter for assessing angiogenic activity. Patients with high IMD
have decreased survival rates in a variety of cancers (Fujioka, S., et al., Cancer, 92: 1788-
1797, 2001). Thymidine phosphorylase (TYPH or TP, Seq ID No. 31) which is identical
to platelet-derived endothelial cell growth factor, is strongly expressed in PC and
30   stimulates the chemotaxis of endothelial cells through the 2-deoxy-D-ribose, degradation
products of thymidine by TP, thus indirectly inducing angiogenesis (Haraguchi, M., et al.
Nature, 368: 198, 1994.). Shuichi Fujioka et al. found that IMD and TP status were
independent predictive indicators for overall as well as relapse-free survival in PC
(Fujioka, S., et al., Cancer, 92: 1788-1797, 2001). An additional protein detected at higher
35   levels in PC than in surrounding tissue likely involved in metastasis formation is

osteoblast specific factor 2 (Seq ID No.53), a putative bone adhesion protein. Breast carcinoma commonly metastasizes to bone (Guise, T. A. Cancer, *88*: 2892-2898, 2000). Although the role of this protein in PC is not clearly established, our findings suggest a similar role for osteoblast specific factor 2 in PC. Thus, a preferred embodiment of the

5   present invention is a marker comprising Seq ID. No. 31. In another preferred embodiment, the marker comprises Seq. ID No. 53.

Small GTP-binding proteins

Four small GTP-binding proteins and interacting proteins were more strongly expressed in PC than in normal pancreas tissue. These include RAN (Seq. ID No. 27),

10   GBLP (guanine nucleotide binding protein β subunit-like protein RACK1, Seq. ID No. 47), GDIR (Rho GDP dissociation inhibitor 1, Seq. ID No. 55), and IQG1 or IQGAP1 (Ras gtpase activating like protein, Seq ID No. 25). Small GTP-binding proteins constitute a superfamily, which is structurally classified into at least five families: the Ras, Rho, Rab, Sar1/Arf, and Ran families and are involved in the regulation of gene

15   expression, cytoskeletal reorganization, and nucleocytoplasmic transport (Takai, Y., et al. Physiol Rev., *81*: 153-208, 2001). RAN is known to enhance androgen receptor-mediated transactivation and was shown to be overexpressed in prostate cancer (Sampson, E. R., et al., J.Biol.Regul.Homeost.Agents, 15: 123-129, 2001). Increased expression of RAN in 81% of prostate tumor cases, may contribute to over proliferation of prostate tumor cells

20   (Li, P., et al., Am J Pathol., 161: 1467-1474,2002). GBLP is an anchoring protein for activated protein kinase Cβ and a variety of other proteins. Protein kinase C plays an important role in angiogenesis and cancer growth. Berns et al. found GBLP up-regulated in during angiogenesis *in vitro* and also associated with nonendothelial cells in angiogenically active tissue (Berns, H., et al., FASEB J., *14*: 2549-2558, 2000). Further

25   more, mRNA expression of GBLP is detected in epithelial cells of human colon carcinoma and proliferating epithelial cell of normal colon tissue. Therefore, there is a likely link between high GBLP expression and tumor growth. GDIR (Rho GDP dissociation inhibitor) had been found up-regulated in a chemoresistant fibrosarcoma cell line by 2D-PAGE (Sinha, P., et al., Electrophoresis, *20*: 2961-2969, 1999) and may

30   block apoptotic signal pathway mediated by Ras and c-jun kinase, resulting in the increase resistance against environmental stress. IQG1 (Ras GTPase-activating-like protein) is a widely expressed 190-kDa Cdc42-, Rac1-, and calmodulin-binding protein that interacts with F-actin in vivo and that can cross-link F-actin microfilaments in vitro. IQG1 negatively regulates the Ecc-based (E-cadherin/catenin complex) cell-cell adhesion

35   by dissociating alpha-catenin. Up-regulation of IQGAP1 is correlated with the malignant

phenotype in gastric cancer (Sugimoto, N., et al., J. Hum. Genet., 46: 21-25, 2001). By immunohistochemical analysis, IQGAP1 was found overexpressed in colorectal carcinoma and associated with carcinoma invasion (Nabeshima, K., et al., Cancer Lett., 176: 101-109, 2002). Since cancer invasiveness is associated with the localized disruption

5   of cell-cell adhesion, both our results and Iacobuzio-Donahue et al.'s data suggest that IQGAP1 may be involved in the disruption of local adhesion and in PC invasion to surrounding tissue. Thus, a preferred embodiment of the present invention is a marker comprising Seq ID No. 27. In another preferred embodiment, the marker comprises Seq. ID No. 47. In another preferred embodiment, the marker comprises Seq. ID No. 55. In

10 another preferred embodiment, the marker comprises Seq. ID No. 25.

   ### S100 protein family

       Another protein with high-level expression in PC is S109 (S100A9, MRP-14, calgranulin B, Seq ID No. 49), a member of the S100 protein family of highly homologous low molecular weight calcium binding proteins. Calgranulins are

15 characterized by cell type-specific expression in cells of epithelial, myeloid and endothelial origin and accumulation at sites of acute and chronic inflammation (e.g. rheumatoid arthritis, cystic fibrosis, psoriasis, allergic dermatitis, inflammatory bowel diseases) (Donato, R. Int.J.Biochem.Cell Biol., 33: 637-668, 2001). S100A8 and S100A9 can form a noncovalent heterodimer protein complex called calprotectin. Current

20 reports support that both of S100A9 and S100 A8 have wide range of possible intracellular as well as extracellular functions (Schafer, B. W. and Heizmann, C. W. Trends Biochem.Sci., 21: 134-140, 1996). S100A8 and S100A9 are negatively regulated by glucocorticoids in a c-Fos-dependent manner and over expressed throughout skin carcinogenesis (Gebhardt, C., et al., Oncogene, 21: 4266-4276, 2002). These proteins are

25 also more strongly expressed in colorectal carcinoma than in matched normal colon mucosa, as shown by proteomics analysis (Stulik, J., et al., Electrophoresis, 20: 1047-1054, 1999). S100A9 has been detected in cultured human adenocarcinoma (AC) cells derived from various organs, and is associated with tumor differentiation in pulmonary adenocarcinoma (Arai, K., et al., Oncol.Rep., 8: 591-596, 2001). Iacobuzio-Donahue et

30 al's work indicates that over expression of S100A4 in PC is associated with poor differentiation and DNA hypomethylation (Rosty, C., et al., Am.J.Pathol., 160: 45-50, 2002). Thus, a preferred embodiment of the present invention is a marker comprising Seq ID. No. 49.

   ### Annexin

We found that annexin 1 (Seq ID No. 51) and annexin 2 (Seq ID No. 19) have high level of expression in PC. Both are members of a family of Ca^{2+}-dependent membrane-binding proteins. Described functions include, among others, an important role in malignant transformation (Masaki, T., et al., Hepatology, *24*: 72-81, 1996), the control of

5   epithelial cell line proliferation (Solito, E., et al., Cell Growth Differ., *9*: 327-336, 1998), and mediation of apoptosis (Canaider, S., et al.,. Life Sci., *66*: L265-L270, 2000). Evidence in support of causative roles for any annexins in the development of cancer is still mainly circumstantial. In MCF-7 breast carcinoma cells, overexpression of annexin1 led to abrogation of Ca2+ release after activation of purinergic or bradykinin receptors (Frey, B.

10   M., et al., FASEB J., *13*: 2235-2245, 1999), while over expression of annexin1 in rat 2 fibroblasts leads to direct inhibition of cytosolic PLA2, which in turn depresses the serum response element of c-fos (Oh, J., et al., FEBS Lett., *477*: 244-248, 2000). Collectively, these studies imply a growth-suppressive role for annexin1. These results are not supported by the finding that annexin 1 is strongly up-regulated in a prostate cancer cell

15   line (Vaarala, M. H., Lab Invest, *80*: 1259-1268, 2000), esophageal cancer (Emmert-Buck, M. R., et al., Mol.Carcinog., *27*: 158-165, 2000), a stomach cancer cell line (Sinha, P., et al., J.Biochem.Biophys.Methods, *37*: 105-116, 1998), mammary adenocarcinoma (Pencil, S. D. and Toth, M. Clin.Exp.Metastasis, *16*: 113-121, 1998), and hepatocarcinoma (de Coupade, C., et al., Hepatology, *31*: 371-380, 2000). In hepatocarcinoma, study also

20   showed that the proliferative rate of both normal and malignant hepatocytes was attenuated by antisense to annexin 1. These and our data suggest that cell growth is associated with elevated rather than reduced levels of annexin 1, which is also supported by the studies of Iacobuzio- Donahue et al. (Am. J. Pathol., *160*: 1239-1249, 2002). Thus, a preferred embodiment of the present invention is a marker comprising Seq ID No. 51.

25   In another preferred embodiment, the marker comprises Seq. ID No. 19.

Some additional proteins highly expressed in PC may have either clear roles in PC or an indirect link with PC, e.g. BGH3 (TGF-β1-induced protein, Seq ID No. 6) which is a secretory protein and acts as a marker for biologically active TGF- β 1 (Langham, R. G.,

30   et al., Transplantation, *72*: 1826-1829, 2001). Thus, a preferred embodiment of the present invention is a marker comprising Seq ID No. 6.

With the identification of polypeptides regulated in pancreatic cancer, the present invention provides an in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of obtaining a biological sample; and detecting and/or measuring the increase of a marker described hereinbefore. The term "detection" as used herein refers to the qualitative determination of the absence or presence of polypeptides. The term "measured" as used herein refers to the quantitative determination of the differences in expression of polypeptides in biological samples from patients with pancreatic cancer and biological samples from healthy individuals. Methods for detection and/or measurement of polypeptides in biological samples are well known in the art and include, but are not limited to, Western-blotting, ELISAs or RIAs . Antibodies recognizing the polypeptides listed in table 2, 3, 5 and/or 6 can either be generated for the purpose of detecting said polypeptides, eg. by immunizing rabbits with purified proteins, or known antibodies recognizing said polypeptides can be used. For example, an antibody capable of binding to the denatured proteins, such as a polyclonal antibody, can be used to detect the peptides of this invention in a Western Blot. An example for a method to measure a marker is an ELISA. This type of protein quantitation is based on an antibody capable of capturing a specifc antigen, and a second antibody capable of detecting the captured antigen. A further method for the detection of a diagnostic marker for pancreatic cancer is by analysing biopsy specimens for the presence or absence of the markers of this invention. Methods for the detection of these markers are well known in the art and include, but are not limited to, immunohistochemistry or immunofluorescent detection of the presence or absence of the polypeptides of the marker of this invention. Methods for preparation and use of antibodies, and the assays mentioned hereinbefore are described in Harlow, E. and Lane, D. Antibodies: A Laboratory Manual, (1988), Cold Spring Harbor Laboratory Press.

The accuracy of the diagnosis of pancreatic cancer can be increased by analysing combinations of multiple polypeptides listed in tables table 2, 3, 5 and/or 6. Thus, the in vitro method herein before described, comprises a marker which comprises at least two, preferably at least three, more preferably at least four, even more preferably at least five, and most preferably at least six of the polypeptides listed in table 2,3, 5 and/or 6.

For diagnosis of pancreatic cancer, suitable biological samples need to be analysed for the presence or absence of a marker. Said biological samples can be serum, plasma,

pancreatic juice or cells of pancreatic tissue. Cells from pancreatic tissue can be obtained by ERCP, secretin stimulation, fine-needle aspiration, cytologic brushings and large-bore needle biopsy.

5   It is also possible to diagnose pancreatic cancer by detecting and/or measuring nucleic acid molecules coding for the marker hereinbefore described. Preferably, said nucleic acid molecule is RNA or DNA. In another embodiment, said DNA is a cDNA.

10   In one embodiment of the present invention, the in vitro method herein before described comprises comparing the expression levels of at least two of the nucleic acids encoding said polypeptides in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer, to the expression levels of the same nucleic acids in a healthy individual.

15   In another embodiment of the present invention the in vitro method herein before described comprises comparing the expression level of said marker in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer to the expression levels of the same marker in a healthy individual. In a more preferred embodiment of the in vitro method, an increase or decrease of the expression levels of
20   said marker is indicative of pancreatic cancer or the susceptibility to pancreatic cancer.

The present invention also provides a screening method for identifying and/or obtaining a compound which interacts with a polypeptide listed in table 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of contacting
25   said polypeptide with a compound or a plurality of compounds under conditions which allow interaction of said compound with said polypeptide; and detecting the interaction between said compound or plurality of compounds with said polypeptide.

The "interaction" in the screening methods as disclosed herein may be measured by
30   conventional methods. The type of conventional method for testing the interaction of a

compound with a polypeptide that is soluble, as opposed to membrane associated, can be an in vitro method using either purified recombinant polypeptide, or native polypeptide purified from cells that endogenously express the polypeptide. As a non-limiting example, a polypeptide of the invention can be bound to beads or immobilized on plastic
5   or other surfaces, and interaction of a compound with the polypeptide can be measured by either using a labelled compound and measuring the label bound to the polypeptide or by displacement of a labeled known ligand from said polypeptide.

For polypeptides that are associated with the cell membrane on the cell surface, or
10 which are expressed as transmembrane or integral membrane polypeptides, the interaction of a compound with said polypeptides can be detected with different methods which include, but are not limited to, methods using cells that either normally express the polypeptide or in which the polypeptide is overexpressed, eg. by detecting displacement of a known ligand which is labeled by the compound to be screened.
15 Alternatively, membrane perparations may be used to test for interaction of a compound with such a polypeptide

Interaction assays to be employed in the method disclosed herein may comprise FRET-assays (fluorescence resonance energy transfer; as described, inter alia, in Ng,
20 Science 283 (1999), 2085-2089 or Ubarretxena-Belandia, Biochem. 38 (1999), 7398-7405), TR-FRETs and biochemical assays as disclosed herein. Furthermore, commercial assays like "Amplified Luminescent Proximity Homogenous Assay^{TM}" (BioSignal Packard) may be employed. Further methods are well known in the art and, inter alia, described in Fernandez, Curr. Opin. Chem. Biol. 2 (1998), 547-603.

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The "test for interaction" may also be carried out by specific immunological and/or biochemical assays which are well known in the art and which comprise, e.g., homogenous and heterogenous assays as described herein below. Said interaction assays employing read-out systems are well known in the art and comprise, inter alia, two-
30 hybrid screenings (as, described, inter alia, in EP-0 963 376, WO 98/25947, WO 00/02911; and as exemplified in the appended examples), GST-pull-down columns, co-precipitation assays from cell extracts as described, inter alia, in Kasus-Jacobi, Oncogene 19 (2000), 2052-2059, "interaction-trap" systems (as described, inter alia, in US

6,004,746) expression cloning (e.g. lamda gt11), phage display (as described, inter alia, in US 5,541,109), in vitro binding assays and the like. Further interaction assay methods and corresponding read out systems are, inter alia, described in US 5,525,490, WO 99/51741, WO 00/17221, WO 00/14271 or WO 00/05410. Vidal and Legrain (1999) in Nucleic

5   Acids Research 27, 919-929 describe, review and summarize further interaction assays known in the art which may be employed in accordance with the present invention.

Homogeneous (interaction) assays comprise assays wherein the binding partners remain in solution and comprise assays, like agglutination assays.

10   Heterogeneous assays comprise assays like, inter alia, immuno assays, for example, Enzyme Linked Immunosorbent Assays (ELISA), Radioactive Immunoassays (RIA), Immuno Radiometric Assays (IRMA), Flow Injection Analysis (FIA), Flow Activated Cell Sorting (FACS), Chemiluminescent Immuno Assays (CLIA) or Electrogenerated Chemiluminescent (ECL) reporting.

15

The present invention further provides a screening method for identifying and/or obtaining a compound which is an inhibitor or an antagonist of a polypeptide listed in table 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of a) contacting said polypeptide with a compound identified and/or obtained by

20   the screening method described above under conditions which allow interaction of said compound with said polypeptide; b) determining the activity of said polypeptide; c) determining the activity of said polypeptide expressed in the host as defined in (a), which has not been contacted with said compound; and d) quantitatively relating the activity as determined in (b) and (c), wherein a decreased activity determined in (b) in comparison

25   to (c) is indicative for an inhibitor or antagonist. The terms inhibitors and antagonists as used herein are used interchangeably. This screening assay can be performed either as an in vitro assay, or as a host-based assay. The host to be employed in the screening methods of the present invention and comprising and/or expressing a polypeptide listed in table 2, 3, 5 and/or 6 may comprise prokaryotic as well as eukaryotic cells. Said cells may

30   comprise bacterial cells, yeast cells, as well as cultured (tissue) cell lines, inter alia, derived from mammals. Furthermore animals may also be employed as hosts, for example an non-human transgenic animal. Accordingly, said host (cell) may be transfected or transformed with the vector comprising a nucleic acid molecule coding for a polypeptide which is differentially regulated in pancreatic cancer as disclosed herein. Said host cell or

35   host may therefore be genetically modified with a nucleic acid molecule encoding such a

polypeptide or with a vector comprising such a nucleic acid molecule. The term "genetically modified" means that the host cell or host comprises in addition to its natural genome a nucleic acid molecule or vector coding for a polypeptide listed in table 2, 3, 5 and/or 6 or at least a fragment therof. Said additional genetic material may be introduced

5   into the host (cell) or into one of its predecessors/parents. The nucleic acid molecule or vector may be present in the genetically modified host cell or host either as an independent molecule outside the genome, preferably as a molecule which is capable of replication, or it may be stably integrated into the genome of the host cell or host.

10   As mentioned herein above, the host cell of the present invention may be any prokaryotic or eukaryotic cell. Suitable prokaryotic cells are those generally used for cloning like E. coli or Bacillus subtilis. Yet, these prokaryotic host cells are also envisaged in the screening methods disclosed herein. Furthermore, eukaryotic cells comprise, for example, fungal or animal cells. Examples for suitable fungal cells are yeast cells,

15   preferably those of the genus Saccharomyces and most preferably those of the species Saccharomyces cerevisiae. Suitable animal cells are, for instance, insect cells, vertebrate cells, preferably mammalian cells, such as e.g. CHO, HeLa, NIH3T3 or MOLT-4. Further suitable cell lines known in the art are obtainable from cell line depositories, like the American Type Culture Collection (ATCC).

20

The hosts may also be selected from non-human mammals, most preferably mice, rats, sheep, calves, dogs, monkeys or apes. As described herein above, said animals/mammals also comprise non-human transgenic animals, which preferably express at least one polypeptide differentially regulated in pancreatic cancer as disclosed

25   herein. Preferably, said polypeptide is a polypeptide which is up-regulated in tissue derived from patients with pancreatic cancer. Yet it is also envisaged that non-human transgenic animals be produced which do not express marker genes as disclosed herein or who express limited amounts of said marker gene products. Said animals are preferably related to polypeptides which are down-regulated in pancreatic cancer. Transgenic non-

30   human animals comprising and/or expressing the up-regulated polypeptides of the present invention or alternatively, which comprise silenced or less efficient versions of down-regulated polypeptides are useful models for studying the development of pancreatic cancer and provide for useful models for testing drugs and therapeutics for pancreatic cancer treatment and/or prevention.

35

A compound which interacts with a polypeptide listed in table 2, 3, 5 and/or 6 and which inhibits or antagonizes said polypeptide is identified by determining the activity of said polypeptide in the presence of said compound.

5   The term "activity" as used herein relates to the functional property or properties of a specific polypeptide. For the enzymes listed in table 2, 3, 5 and/or 6, the term "activity" relates to the enzymatic activity of a specific polypeptide. Activity assays for the enzymes listed in table 2, 3, 5 and/or 6 are well known.

10   For adhesion molecules listed in table 2, 3, 5 and/or 6, the term "activity" relates to the adhesive properties of a polypeptide and may determined using assays such as, but not limited to, adhesion assays, cell spreading assays, or in vitro interaction of the adhesion molecule with a known ligand. Such assays are well known in the art.

15   For cytoskeletal proteins, the term "activity" relates to the regulation of the cytoskeleton by such polypeptides, or to their incorporation into the cytoskeleton. As a non-limiting example, the ability of Gelsolin to regulate actin polymerization, or of Filamin A to promote orthogonal branching of actin filaments, may be determined using in vitro actin polymerization assays. Activity in relation to the regulation of cytoskeletal
20   structures may further be determined by, as non-limiting examples, cell spreading assays, cell migration assays, cell proliferation assays or immunofluorecence assays, or by staining actin filaments with fluorescently labeled phalloidin. All of these assays are well known to the person skilled in the art.

25   For ion channels (Chloride intracellular channel protein) the term "activity" relates to ion flux (Chloride lux) across the membrane. Methods to determine ion flux across membranes are well known to the person skilled in the art.

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For transcription factors, eg. KIAA 1034, the term "activity" relates to their ability to regulate gene transcription. The transcriptional activity of a polypeptide can be determined using commonly used assays, such as a reporter gene assay.

5   For growth factors and hormones or their receptors, the term "activity" relates to their ablitiy to bind to their receptors or ligands, respectively, and to induce receptor activation and subsequent signaling cascades, and/or it relates to the factor's or receptor's ability to mediate the cellular function or functions eventually caused by growth factor or hormone mediated receptor activation. Growth factor or hormone binding to receptors

10   can be determined by commonly known ligand binding assays. Receptor activation can be determined by testing for receptor auto-phosphorylation, or by assaying for modification or recruitment of downstream signaling mediators to the receptors (by immunoprecipitation and Western Blotting of signaling complexes). Cellular functions regulated by growth factors or hormones and their receptors can be cell proliferation (eg

15   determined by using thymidine incorporation or cell counts), cell migration assays (eg determined by using modified Boyden chambers), cell survival or apoptosis assays (eg determined by using DAPI staining), angiogenesis assays (eg in vitro assays to measure endothelial tube formation that are commercially available). In addition to these assays, other assays may be used as well to determine these and other cellular functions.

20

Inhibitors or antagonists of a polypeptide listed in tables 2 and/or 3 are identified by the screening method described above when there is a decreased activity determined in the presence of the compound in comparison to the absence of the compound in the screening method, which is indicative for an inhibitor or antagonist.

25

Further to the screening methods disclosed above, this invention provides a screening method for identifying and/or obtaining a compound which is an inhibitor of the expression of a polypeptide listed in tables 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of a) contacting a host which expresses said

30   polypeptide with a compound; b) determining the expression level and/or activity of said polypeptide; c) determining the expression level and/or activity of said polypeptide in the host as defined in (a), which has not been contacted with said compound; and d) quantitatively relating the expression level of said polypeptide as determined in (b) and

(c), wherein a decreased expression level determined in (b) in comparison to (c) is indicative for an inhibitor of the expression of said polypeptide.

An inhibitor of the expression of a polypeptide listed in table 2, 3, 5 and/or 6
5   is identified by the screening method described hereinbefore when a decreased expression of the protein is determined in the presence of the compound in comparison to the absence of the compound in the screening method, which is indicative for an inhibitor of expression of a polypeptide.

10   The term "express" as used herein relates to expression levels of a polypeptide listed table 2, 3, 5 and/or 6 which is up-regulated in pancreatic cancer, in cells, preferably in a pancreatic adenocarcinoma cell line, which are elevated as compared to the expression levels of the same polypeptide in healthy pancreatic cells. Preferably, expression levels are at least 2 fold, more preferably at least 3 fold, even more preferably
15 at least 4 fold, most preferably at least 5 fold higher than in healthy pancreatic cells.

Furthermore, the present invention provides a compound identified and/or obtained by any of the screening methods hereinbefore described. Said compound is further comprised in a pharmaceutical composition. A method for the preparation of
20 said pharmaceutical composition comprising formulating said compound in a pharmaceutically acceptable carrier or diluent is also claimed. Any conventional carrier material can be utilized. The carrier material can be an organic or inorganic one suitable for eteral, percutaneous or parenteral administration. Suitable carriers include water, gelatin, gum arabic, lactose, starch, magnesium stearate, talc, vegetable oils, polyalkylene-
25 glycols, petroleum jelly and the like. Furthermore, the pharmaceutical preparations may contain other pharmaceutically active agents. Additional additives such as flavoring agents, stabilizers, emulsifying agents, buffers and the like may be added in accordance with accepted practices of pharmaceutical compounding.

30   Said compound may be used for the preparation of a medicament for the treatment or prevention of pancreatic cancer. In addition, said compound may also be used for the preparation of a diagnostic composition for diagnosing pancreatic cancer or a predisposition for pancreatic cancer. Preferably, said compound comprises an antibody, an antibody-derivative, an antibody fragment, a peptide or an antisense
35 construct.

Within the scope of the present invention, antibodies against the proteins listed in tables 2 and/or 3, or antigen-binding fragments thereof, may be used in an in vitro method for the diagnosis of pancreatic cancer.

5   In order to efficiently perform diagnostic screenings, the present invention provides a kit for the diagnosis of pancreatic cancer comprising one or more of the antibodies, or antigen-binding fragments thereof, described above. Another kit provided by this invention is a kit for the diagnosis of pancreatic cancer comprising one or more of the nucleic acids coding for the marker hereinbefore described. Yet another kit provided
10   by this invention is a kit for screening of compounds that antagonize any of the polypeptides listed in tables 2 and/or 3 or inhibit the expression of any of said polypeptides.

The present invention pertains to a marker for diagnosis of pancreatic cancer
15   comprising at least one polypeptide selected from the group consisting of the polypeptides listed in table 6. Preferably, said marker does not include Seq ID No.s 25 and 50 to 55. In a more preferred embodiment, said marker comprises at least one of the polypeptides listed in table 5.

The present invention also provides an in vitro method for the diagnosis of
20   pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of

        a) obtaining a biological sample; and

        b) detecting and/or measuring the increase of at least one of the polypeptides listed in table 6.

Preferably, said in vitro method additionally comprises the step of detecting and/or
25   measuring the decrease of at least one of the polypeptides listed in table 5. More preferably, in said vitro method, said at least one polypeptide does not include Seq ID No.s 25 and 50 to 55. Even more preferably, in said vitro method, said biological sample is derived from the group consisting of serum, plasma, pancreatic juice and cells of pancreatic tissue.

30

The present invention further provides an in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of

a) obtaining a biological sample; and

b) detecting and/or measuring the increase of at least one nucleic acid coding for the marker hereinbefore described.

Preferably, in said in vitro method, said nucleic acid molecule is RNA or DNA. More preferably, in said in vitro method, said DNA is a cDNA.

In a further more preferred embodiment of any of the in vitro methods hereinbefore described, the expression levels of at least one of said nucleic acids in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same nucleic acids in a healthy individual. In a most preferred embodiment of any of the in vitro methods hereinbefore described, the expression level of said marker in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same marker in a healthy individual.

In a further preferred embodiment of the in vitro method hereinbefore described, an increase of the expression levels of said marker is indicative of pancreatic cancer or the susceptibility to pancreatic cancer.

The present invention also pertains to a screening method for identifying and/or obtaining a compound which interacts with a polypeptide selected from the group consisting of the polypeptides listed in table 6 whose expression is upregulated in pancreatic cancer, comprising the steps of

a) contacting said polypeptide with a compound or a plurality of compounds under conditions which allow interaction of said compound with said polypeptide; and

b) detecting the interaction between said compound or plurality of compounds with said polypeptide.

Furthermore, the present invention provides a screening method for identifying and/or obtaining a compound which is an inhibitor or an antagonist of a polypeptide listed in table 6 whose expression is upregulated in pancreatic cancer, comprising the steps of

a) contacting said polypeptide with a compound identified and/or obtained by the screening method of claim 39 under conditions which allow interaction of said compound with said polypeptide;

b) determining the activity of said polypeptide;

c) determining the activity of said polypeptide expressed in the host as defined in (a), which has not been contacted with said compound; and

d) quantitatively relating the activity as determined in (b) and (c), wherein a decreased activity determined in (b) in comparison to (c) is indicative for an inhibitor or antagonist.

The present invention also provides a screening method for identifying and/or obtaining a compound which is an inhibitor of the expression of a polypeptide selected from the group consisting of the polypeptides listed in table 6 whose expression is upregulated in pancreatic cancer, comprising the steps of

a) contacting a host which expresses said polypeptide with a compound,

b) determining the expression level and/or activity of said polypeptide;

c) determining the expression level and/or activity of said polypeptide in the host as defined in (a), which has not been contacted with said compound; and

d) quantitatively relating the expression level of said polypeptide as determined in (b) and (c), wherein a decreased expression level determined in (b) in comparison to (c) is indicative for an inhibitor of the expression of said polypeptide.

The present invention provides a compound identified and/or obtained by the screening methods hereinbefore described.

In addition, the present invention provides a pharmaceutical composition comprising the compound hereinbefore described. Also provided is a method for the preparation of the pharmaceutical composition hereinbefore described comprising formulating the compound hereinbefore described in a pharmaceutically acceptable carrier or diluent.

The present invention provides a use of a compound hereinbefore described for the preparation of a medicament for the treatment or prevention of pancreatic cancer. Also provided is a use of a compound hereinbefore described for the preparation of a diagnostic composition for diagnosing pancreatic cancer or a predisposition for

5   pancreatic cancer. In a preferred embodiment, the uses hereinbefore described relate to a compound comprising an antibody, an antibody-derivative, an antibody fragment, a peptide or an antisense construct.

Within the scope of the present invention, antibodies against the proteins

10   listed in tables 5 and/or 6, or antigen-binding fragments thereof, may be used in an in vitro method for the diagnosis of pancreatic cancer.

In order to efficiently perform diagnostic screenings, the present invention provides a kit for the diagnosis of pancreatic cancer comprising one or more of the

15   antibodies, or antigen-binding fragments thereof, described above. Another kit provided by this invention is a kit for the diagnosis of pancreatic cancer comprising one or more of the nucleic acids coding for the marker hereinbefore described. Yet another kit provided by this invention is a kit for screening of compounds that antagonize any of the polypeptides listed in tables 5 and/or 6 or inhibit the expression of any of said

20   polypeptides.

In the present invention, the proteins, compounds, kits, methods and uses substantially as herein before described, especially with reference to the foregoing

25   examples are also claimed.

Examples:

Collection of tissue samples

5   Pancreatic carcinomas and adjacent tissue were collected from the patients listed in
table 1.

Samples were collected shortly after the resection (less than 30 minutes), and fast frozen
in liquid nitrogen for about 1 minute, then stored in a freezer at a temperature of –80°C.

10   Characterization of formalin-fixed specimens

Histopathological characterization was carried out by using hematoxylin-eosin-
stained sections of formalin-fixed and paraffin-embedded specimens. Tumors were
classified using the WHO system. The types of pancreatic carcinomas included in the
study are shown in table 1.

15

The twelve pancreatic carcinoma samples used in this study were ductal carcinomas
which constitute the overwhelming proportion of pancreatic carcinomas. The patient-
matched samples from histologically normal tissue surrounding the carcinoma were used
as controls. We carried out 12 pairs of 2-dimensional electrophoresis maps for
20   comparing protein expression between tumor tissue and normal control tissue. For
protein identification, the samples were pooled, thus generating pan-Carcinoma and
pan-Normal protein extracts. Quantification was carried out in two steps: (I) Gels from
the pooled samples were compared using the PDQuest image analysis software. (II) The
changes identified at the level of the pooled samples were cross-validated by an analysis of
25   the individual samples. The change factors shown in table 2, 3, 5 and 6 were determined
using the pooled samples.

Preparation of samples for electrophoresis

Samples cleaned of clots and contaminating tissue were frozen in liquid nitrogen, then ground to powder. Samples were suspended in lysis buffer (8M urea, 4% CHAPS, 40mMol/L Tris-Cl, 0.5% carier amphollytes, 100mMol/L DTT and 0.1ìg/ìl PMSF) and

5   centrifuged at 12000rpm for 30 minutes. The supernatants were stored at –80°C. The protein concentration in the extracts was determined by the Bradford method (Bradford, M. Anal. Biochem. 72, 248 (1976).

Two-dimensional gel electrophoresis

10   Samples containing 1 mg of protein were loaded onto the rehydrated IPG strip (18 cm, pH3~10) by using the cup loading method. IEF was performed using Pharmacia Multiphor apparatuses under the following conditions: First, the voltage was increased 200V-5000V over 24hrs, then a constant voltage of 5000V was applied for 24 hrs, the running temperature was 20°C. After IEF, the strips were equilibrated with 10 ml

15   equilibration solution I (6 M Urea, 50 mM Tris pH 8.8, 30 % Glycerol, 2.0 % SDS, 30 mM Dithioerythritol) for 15 min, then for another 15 min with equilibration solution II (6 M Urea, 50 mM Tris pH 8.8, 30 % Glycerol, 2.0 % SDS, 0.23 M Iodoacetamide).

The second dimension SDS polyacrylamide gel electrophoresis (SDS-PAGE) was

20   carried out using a Hoefer ISO_DALT apparatus (10 gels/run, 24×20 cm), IEF strips were loaded onto 12% homogeneous polyacrylamide gels (1.5 mm x 24 cm × 20 cm). The gels were run in TGS_Buffer (250 mM Tris, 1.92 M Glycine, 1% (w/v) SDS, pH = 8.3, Bio-Rad) at a constant voltage (80 V, 20°C).

25   Gel fixation and staining

Gels were fixed in 50% Methanol/20% acetic acid for 30 min, then washed in ultra-pure water for 30 min and stained with NOVEX Colloidal Blue staining Kit (Invitrogen) following the manufacturer's recommendations.

Protein Identification

The protein identification was performed using a two-step procedure.

In-gel digestion

5   Spots were picked and transferred into 96-well by a spot picking robot. From each gel, 600-800 spots were picked. The spots were destained with 100µl of 30% acentonitrile in 50Mm ammonium bicarbonate, washed in ultra pure-water and dried in a speed vac evaporator. The dry gel pieces were digested with 10ng/µl trypsin (Promega, Madison, USA) solution in 500 nM ammonium bicarbonate at room temperature for 16 h

10   maximum. The peptides from each spot were extracted with 20µl of 0.1% trifluore acetic acid (TFA) in 50% acetonitrile. The matrix solution consisted of 0.025%(w/v) alfa-cyano-4-hydroxy cinammic acid (Sigma) in 50% acetonitrile/0.1% TFA with internal standard peptides des-Arg-Bradykinin(Sigma, MW 904.4681 Da) and adrenocorticotropic hormone fragment 18-39 (Sigma, MW 2465.1989 Da).

15

Analysis by MALDI-TOF

       1.5ul of peptide extract and 1.0µl of matrix solution were stimulaneously applied to the spots on the MS target. Recrytallization was carried out as specified by the instruments manufacturer. The samples were analyzed in a MALDI-time of flight Mass

20   spectrometer (Autoflex, Bruker Analytics, Bremen, Germany). Peak annotation and database search by peptide matching was performed by in house developed software. The peptide mass was compared with theoretic peptide masses of all available proteins from all species. The monoisotopic mass was used and a mass tolerence of 0.0025% was allowed. 4 matching peptides were the minimal requirement for an identity assigment.

25   Mismatch or miscleavage sites were not considered.

Table 1: Clinical and histopathological characteristics of samples

No. of Samples	Sex	Age	Tumor location	Histology	Metastasis in lymph nodes
PC-01	Male	48	Head of pancreas	Middle differentiated ductal adenocarcinoma	Yes
PC-02	Male	68	Head of pancreas	Poorly differentiated adenocarcinoma	Yes
PC-03	Male	44	Head of pancreas	Poorly differentiated ductal adenocarinoma, clear cell type	Yes
PC-04	Male	66	Head of pancreas	Well differentiated ductal adenocarcinoma	Yes
PC-05	Female	45	Head of pancreas	Well differentiated ductal adenocarcinoma	No
PC-06	Female	65	Head of pancreas	Well differentiated ductal adenocarcinoma	Yes
PC-07	Male	59	Head of pancreas	Middle differentiated ductal adenocarcinoma	Yes
PC-08	Female	62	Body of pancreas	Well differentiated ductal adenocarcinoma	Yes
PC-09	Male	54	Head of pancreas	Middle differentiated ductal adenocarcinoma	No
PC-10	Female	53	Head of pancreas	Well differentiated ductal adenocarcinoma	No
PC-11	Female	54	Head of pancreas	Middle differentiated ductal adenocarcinoma	Yes
PC-12	Female	69	Head of pancreas	Middle differentiated ductal adenocarcinoma	Yes

Table 2: Proteins up-regulated in pancreatic cancer I

Protein	Acc No	Description	Seq ID No.	Fold Change
sw:CATD_HUMAN	P07339	Cathepsin D precursor (ec 3.4.23.5).	1	<2
sw:IDHC_HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic (ec 1.1.1.42)	2	2
sw:GELS_HUMAN	P06396	Gelsolin precursor, plasma	3	3
sw:CFAB_HUMAN	P00751	Complement factor B precursor (ec 3.4.21.47)	4	5
sw:AAC4_HUMAN	O43707	Alpha-actinin 4 (non-muscle alpha-actinin 4)	5	2
sw:AAC1_HUMAN	P12814	Alpha-actinin 1 (alpha-actinin cytoskeletal isoform)	7	2
sw:TBA4_HUMAN	P05215	Tubulin alpha-4 chain.	8	2
sw:ABP2_HUMAN	P21333	Filamin A (Endothelial actin-binding protein)	9	4
sw:TAGL_HUMAN	P37802	Transgelin 2 (smooth muscle protein 22-alpha)	10	2
sw:TPM4_HUMAN	P07226	Tropomyosin alpha 4 chain	11	<2
sw:BGH3_HUMAN	Q15582	Transforming growth factor-beta induced protein IG-H3 precursor	6	5
sw:CALD_HUMAN	Q05682	Caldesmon (cdm)	12	2
sw:ENOL_HUMAN	Q05524	Alpha enolase	13	2
sw:ACY1_HUMAN	Q03154	Aminoacylase-1	14	5
sw:CAPB_HUMAN	P47756	F-actin capping protein beta subunit (capz beta)	15	5
sw:IPYR_HUMAN	Q15181	Inorganic pyrophosphatase	16	<2
sw:LEG3_HUMAN	P17931	Galectin-3 (galactose-specific lectin 3).	17	2

sw:POR2_HUMAN	P45880	Voltage-dependent anion-selective channel protein 2	18	<2
SW:ANX2_HUMAN	P07355	Annexin II	19	2
sw:CBP2_HUMAN	P50454	Collagen-binding protein 2 precursor	20	2
sw:COF1_HUMAN	P23528	Cofilin, non-muscle isoform	21	<2
sw:CYPH_HUMAN	P05092	Peptidyl-prolyl cis-trans isomerase A	22	<2
sw:DYI2_HUMAN	Q13409	Dynein intermediate chain 2, cytosolic	23	2
sw:ECH1_HUMAN	Q13011	Delta3,5-Delta2,4-dienoyl-coa isomerase, mitochondrial precursor	24	2
sw:MLRN_HUMAN	P24844	Myosin regulatory light chain 2	48	2
sw:PLSL_HUMAN	P13796	L-Plastin	26	<2
sw:RAN_HUMAN	P17080	GTP-binding nuclear protein ran	27	3
sw:ROK_HUMAN	Q07244	Heterogeneous nuclear ribonucleoprotein k	28	2
sw:TCTP_HUMAN	P13693	Translationally controlled tumor	29	<2
sw:TPM1_HUMAN	P09493	Tropomyosin 1 alpha chain	30	<2
sw:TYPH_HUMAN	P19971	Thymidine phosphorylase precursor	31	5
sw:AMPL_HUMAN	P28838	Cytosol aminopeptidase	32	3
sw:K1CS_HUMAN	P08727	Keratin, type i cytoskeletal 19 (cytokeratin 19)	33	4
sw:ALDX_HUMAN	P14550	Alcohol dehydrogenase [NADP+]	34	4
sw:EL3A_HUMAN	P09093	Elastase IIIa precursor	35	4
sw:DLDH_HUMAN	P09622	Dihydrolipoamide dehydrogenase, mitochondrial precursor	36	2
sw:ECHM_HUMAN	P30084	Enoyl-CoA hydratase, mitochondrial precursor	37	3
sw:HSBX_HUMAN	O14558	Heat-shock 20 kDa like-protein p20.	38	2

sw:MLEN_HUMAN	P16475	Myosin light chain alkali, non-muscle isoform	39	3
sw:CALX_HUMAN	P27824	Calnexin precursor	40	3
sw:MA32_HUMAN	Q07021	Complement component 1	41	<2
sw:NUAM_HUMAN	P28331	NADH-ubiquinone oxidoreductase 75 kda subunit, mitochondrial precursor	42	2
sw:PBEF_HUMAN	P43490	Pre-B cell enhancing factor precursor.	43	2
sw:RET1_HUMAN	P09455	Retinol-binding protein I, cellular	44	2
sw:TCPG_HUMAN	P49368	T-complex protein 1, gamma subunit	45	2
sw:RINI_HUMAN	P13489	Placental ribonuclease inhibitor	46	<2
sw:GBLP_HUMAN	P25388	Guanine nucleotide-binding protein beta subunit-like protein 12.3	47	2
sw:S109_HUMAN	P06702	Calgranulin B	49	<2

Table 3: Proteins up-regulated in pancreatic cancer II

Protein	Acc No	Description	Seq ID No	Fold Change
sw:CAPG_HUMAN	P40121	Macrophage capping protein	50	3
sw:ANX1_HUMAN	P04083	Annexin I (lipocortin I) (calpactin II)	51	4
sw:K2C7_HUMAN	P08729	Keratin, type II cytoskeletal 7	52	5
humangp:CHR13-Q15063	Q15063	Osteoblast specific factor 2 precursor	53	2
sw:TGLC_HUMAN	P21980	Protein-glutamine gamma-glutamyltransferase	54	2
sw:GDIR_HUMAN	P52565	Rho GDP-dissociation inhibitor 1	55	<2
sw:IQG1_HUMAN	P46940	Ras GTPase-activating-like protein	25	2

5

Table 4. Proteins roughly classified by their involved biological processing or basic function

Protein function[a]	Number[b]	Percentage (%)[C]
Structural constitural and regulation of cytoskeleton	61	20.8
Cell cycle and metabolism	74	25.3
Response to external stimulus or stress	61	20.8
Signal transduction	13	4.4
Nuclear function	18	6.1
Transport processing	19	6.5
Hemostatis	12	4.1
Cell adhension	7	2.4
Chaperon	7	2.4
Apoptosis	3	1
Unknown function	11	3.7
Others	7	2.4
Total	293	100

Table 5. Proteins with higher levels in normal pancreatic compared to cancer tissue

Protein[a]	AccNo [b]	Description[c]	Fold[d]	Seq ID No.
cytoskeletal regulation				
sw:DESM_HUMAN	P17661	desmin.	3	70
		proteolysis and peptidolysis		
sw:CBPB_HUMAN	P15086	carboxypeptidase b precursor	2	71
sw:CBP1_HUMAN	P15085	carboxypeptidase a1 precursor	Uncalc ulated*	72
sw:CPB2_HUMAN	P50454	carboxypeptidase a2 precursor	Uncalc ulated*	73
sw:CTRB_HUMAN	P17538	chymotrypsinogen b precursor	Uncalc ulated*	74
sw:TRY1_HUMAN	P07477	trypsin i precursor (ec 3.4.21.4) (cationic trypsinogen).	Uncalc ulated*	75
sw:TRY2_HUMAN	P07478	trypsin ii precursor (anionic trypsinogen).	3	76
sw:ILEU_HUMAN	P30740	leukocyte elastase inhibitor	4	77
chaperon				
sw:CH60_HUMAN	P10809	human. mitochondrial matrix protein p1 precursor	2	78
sw:ENPL_HUMAN	P14625	94 kda glucose-regulated protein	3	79
SW:ER29_HUMAN	P30040	endoplasmic reticulum protein erp29 precursor	2	80
sw:PDA2_HUMAN	Q13087	protein disulfide isomerase a2 precursor	2	81
sw:PDA3_HUMAN	P30101	protein disulfide isomerase a3 precursor	2	82
oxidoreductase				
sw:ADHB_HUMAN	P00325	alcohol dehydrogenase beta chain	<2	83
sw:GTO1_HUMAN	P78417	glutathione transferase omega 1	Uncalc ulated*	84
sw:OXRP_HUMAN	Q9Y4L1	150 kda oxygen-regulated protein precursor	Uncalc ulated*	85

sw:PDX4_HUMAN	Q13162	peroxiredoxin 4	<2	86
sw:ULA4_HUMAN	P30039	mawd binding protein	<2	87
metabolism of biological process				
sw:AMYC_HUMAN	P19961	alpha-amylase 2b precursor	3	88
sw:AMYP_HUMAN	P04746	alpha-amylase, pancreatic precursor	Uncalc ulated*	89
sw:ATPA_HUMAN	P25705	atp synthase alpha chain, mitochondrial precursor	<2	90
sw:BAL_HUMAN	P19835	bile-salt-activated lipase precursor	3	91
sw:LIP1_HUMAN	P54315	pancreatic lipase related protein 1 precursor .	<2	92
sw:LIP2_HUMAN	P54317	pancreatic lipase related protein 2 precursor	Uncalc ulated*	93
sw:LIPP_HUMAN	P16233	triacylglycerol lipase, pancreatic precursor	Uncalc ulated*	94
sw:DPY2_HUMAN	Q16555	dihydropyrimidinase related protein-2		95
sw:GABT_HUMAN	P80404	4-aminobutyrate aminotransferase	2	96
sw:GATM_HUMAN	P50440	glycine amidinotransferase, mitochondrial precursor	Uncalc ulated*	97
sw:GR78_HUMAN	P11021	78 kda glucose-regulated protein precursor (grp 78)	3	98
sw:IF32_HUMAN	Q13347	eukaryotic translation initiation factor 3 subunit 2	<2	99
sw:DPY2_HUMAN	Q16555	dihydropyrimidinase related protein-2		100
sw:PGMU_HUMAN	P36871	phosphoglucomutase	2	101
sw:PSA1_HUMAN	P25786	proteasome subunit alpha type 1	2	102
heat shock protein				
sw:HS27_HUMAN	P04792	heat shock 27 kda protein	Uncalc ulated*	103
signaling				
SW:PD6I	Q8WUM4	programmed cell death 6 interacting protein	5	104
muscle development				

hsugp:057687-10-0	Q9bva2	four and a half lim domains 3	<2	105
	Q13643	Skeletal muscle LIM-protein 2 (SLIM 2)(Four and a half LIM domains protein 3)(FHL.3).	<2	106
SW:sli2				
transport of biological process				
sw:CYB5_HUMAN	P00167	cytochrome b5.	2	107
cell adhesion				
sw:PAP1_HUMAN	Q06141	pancreatitis-associated protein 1 precursor.	Uncalc ulated*	108
other				
SW:CA16_HUMAN	P12109	collagen alpha 1(vi) chain precursor.	5	109
SW:LUM_HUMAN	P51884	lumican precursor	3	110

Table 6 Proteins with higher levels in pancreatic cancer compared to in normal tissue

Protein [a]	AccNo[b]	Description[c]	Fold[d]	Seq ID No.
cytoskeletal regulation				
sw:FSC2_HUMAN	O14926	fascin 2 (retinal fascin).	2	56
sw:AAC1_HUMAN	P12814	alpha-actinin 1	2	7
sw:AAC4_HUMAN	O43707	alpha-actinin 4	2	5
sw:ABP2_HUMAN	P21333	endothelial actin-binding protein (alpha-filamin).	4	9
sw:ANX2_HUMAN	P07355	human annexin ii (lipocortin ii)	2	19
sw:CALD_HUMAN	Q05682	caldesmon (cdm).	2	12
sw:CAPB_HUMAN	P47756	f-actin capping protein beta subunit	5	15
sw:CAPG_HUMAN	P40121	macrophage capping protein	3	50
sw:COF1_HUMAN	P23528	cofilin, non-muscle isoform (p18).	<2	21
sw:DEST_HUMAN	P18282	destrin (actin-depolymerizing factor) (adf).	2	57
sw:DYI2_HUMAN	Q13409	dynein intermediate chain 2(fragment).	2	23
sw:GELS_HUMAN	P06396	gelsolin precursor	3	3
sw:K1CS_HUMAN	P08727	keratin, type i cytoskeletal 19	4	33
sw:K2C7_HUMAN	P08729	keratin, type ii cytoskeletal 7	5	52
sw:MLEN_HUMAN	P16475	myosin light chain alkali	3	39
sw:PLSL_HUMAN	P13796	l-plastin (lymphocyte cytosolic protein 1)	<2	26
sw:TAGL_HUMAN	P37802	transgelin (22 kda actin-binding protein).	2	10
sw:TBA4_HUMAN	P05215	tubulin alpha-4 chain.	2	8
proteolysis and peptidolysis				
sw:ACY1_HUMAN	Q03154	aminoacylase-1	5	14
sw:AMPL_HUMAN	P28838	cytosol aminopeptidase	3	32
sw:CATD_HUMAN	P07339	cathepsin d precursor.	<2	1

sw:CFAB_HUMAN	P00751	complement factor b precursor	5	4
sw:EL3A_HUMAN	P09093	elastase iiia precursor	4	35
chaperon				
sw:APE_HUMAN	P02649	apolipoprotein e precursor (apo-e).	<2	59
sw:CALX_HUMAN	P27824	calnexin precursor(p90)	3	40
sw:CYPH_HUMAN	P05092	peptidyl-prolyl cis-trans isomerase a	<2	22
sw:TCPG_HUMAN	P49368	t-complex protein 1, gamma subunit	2	45
sw:CBP2_HUMAN	P50454	human. collagen-binding protein 2 precurso	2	20
tr_hum:Q96C61	Q96C61	hypothetical 88.6 kda protein	5	60
oxidoreductase				
sw:DLDH_HUMAN	P09622	dihydrolipoamide dehydrogenase	2	36
sw:IDHC_HUMAN	O75874	isocitrate dehydrogenase [nadp] cytoplasmic	2	2
sw:NUAM_HUMAN	P28331	nadh-ubiquinone oxidoreductase 75 kda subunit	2	42
metabolism of biological process				
sw:ALDX_HUMAN	P14550	alcohol dehydrogenase [nadp+]	4	34
sw:ECH1_HUMAN	Q13011	delta3,5-delta2,4-dienoyl-coa isomerase	2	24
sw:ECHM_HUMAN	P30084	enoyl-coa hydratase, mitochondrial precursor	3	37
sw:IPYR_HUMAN	Q15181	inorganic pyrophosphatase	<2	16
sw:TYPH_HUMAN	P19971	thymidine phosphorylase precursor	5	31
SW:ENOA_HUMAN	P06733	human alpha enolase	2	61
sw:ENOL_HUMAN	Q05524	alpha enolase, lung specific	2	13
sw:SYW_HUMAN	P23381	tryptophanyl-trna synthetase	2	62
heat shock protein				
sw:HSBX_HUMAN	O14558	heat-shock 20 kda like-protein p20.	2	38
signaling				
sw:GBLP_HUMAN	P25388	guanine nucleotide-binding protein beta subunit-like protein 12.3	2	47

sw:GDIR_HUMAN	P52565	rho gdp-dissociation inhibitor 1	<2	55
sw:IQG1_HUMAN	P46940	ras gtpase-activating-like protein iqgap1	2	25
sw:PBEF_HUMAN	P43490	pre-b cell enhancing factor precursor.	2	43
sw:RAN_HUMAN	P17080	gtp-binding nuclear protein ran	3	27
immune response				
sw:KAC_HUMAN	P01834	ig kappa chain c region.	2	63
sw:MA32_HUMAN	Q07021	pre-mrna splicing factor sf2, p32 subunit.	<2	41
inflammatory reponse				
sw:ANX1_HUMAN	P04083	annexin i (lipocortin i)	4	51
sw:LEG3_HUMAN	P17931	galectin-3	2	17
sw:S109_HUMAN	P06702	calgranulin b (mrp-14)	<2	49
muscle development				
sw:TPM1_HUMAN	P09493	tropomyosin 1 alpha chain	<2	30
sw:TPM4_HUMAN	P07226	tropomyosin alpha 4 chain	<2	11
sw:MLRN_HUMAN	P24844	myosin regulatory light chain 2	2	48
transport of biological process				
humangp:CHR2-Q15092	Q15092	transmembrane protein.	2	64
sw:POR2_HUMAN	P45880	voltage-dependent anion-selective channel protein 2	<2	18
sw:RET1_HUMAN	P09455	retinol-binding protein I	2	44
RNA processing				
humangp:CHR20-Q9P2E9	O75300	ribosome binding protein 1 (kiaa1398 protein).	<2	65
sw:RINI_HUMAN	P13489	placental ribonuclease inhibitor	<2	46
sw:ROK_HUMAN	Q07244	heterogeneous nuclear ribonucleoprotein k	2	28
blood coagulation				
sw:FIBG_HUMAN	P02679	fibrinogen gamma chain precursor	3	66
sw:THRB_HUMAN	P00734	prothrombin precursor	<2	67
Anti-apoptosis				

sw:TCTP_HUMAN	P13693	translationally controlled tumor protein (p23)	<2	29
cell adhesion				
humangp:CHR13-Q15063	Q15063	osteoblast specific factor 2 precursor	2	53
sw:BGH3_HUMAN	Q15582	transforming growth factor-beta induced protein	5	6
other				
sw:TGLC_HUMAN	P21980	tissue transglutaminase	2	54
sw:KPY1_HUMAN	P14618	Human pyruvate kinase, cytosolic thyroid hormone-binding protein	3	68
humangp:CHR19-Q96D15	Q96D15	Reticulocalbin 3 precursor.	2	69

Claims

1.   A marker for diagnosis of pancreatic cancer comprising at least one polypeptide selected from the group consisting of the polypeptides listed in tables 2 and 3.

5   2.   The marker of claim 1 wherein the group from which at least one polypeptide is selected consists of the polypeptides listed in table 2.

3.   A polypeptide selected from the group consisting of the polypeptides listed in tables 2 and 3, for use as a marker or as a component of a marker for diagnosis of pancreatic

10   cancer and/or the susceptibility to pancreatic cancer.

4.   An in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of

       a) obtaining a biological sample; and

15   b) detecting and/or measuring the increase of a marker of claims 1 or 2.

5.   The in vitro method of claim 4, wherein the marker comprises at least two polypeptides.

20   6.   The in vitro method of claims 4 or 5 wherein said biological sample is derived from the group consisting of serum, plasma, pancreatic juice and cells of pancreatic tissue.

7.   An in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of

25   a) obtaining a biological sample; and

       b) detecting and/or measuring the increase of at least one nucleic acid coding for the marker of claims 1 or 2.

8. The in vitro method of claim 7, wherein said nucleic acid molecule is RNA or DNA.

9. The in vitro method of claim 8, wherein said DNA is a cDNA.

5

10. The in vitro method of any one of claims 7 to 9, wherein the expression levels of at least one of said nucleic acids in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same nucleic acids in a healthy individual.

10

11. The in vitro method of any one of claims 4 to 6, wherein the expression level of said marker in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same marker in a healthy individual.

15

12. The in vitro method of claim 11, wherein an increase of the expression levels of said marker is indicative of pancreatic cancer or the susceptibility to pancreatic cancer.

13. A screening method for identifying and/or obtaining a compound which interacts
20 with a polypeptide listed in tables 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of

a) contacting said polypeptide with a compound or a plurality of compounds under conditions which allow interaction of said compound with said polypeptide; and

25 b) detecting the interaction between said compound or plurality of compounds with said polypeptide.

14. A screening method for identifying and/or obtaining a compound which is an inhibitor or an antagonist of a polypeptide listed in tables 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of

   a) contacting a said polypeptide with a compound identified and/or obtained by the screening method of claim 13 under conditions which allow interaction of said compound with said polypeptide;

   b) determining the activity of said polypeptide;

   c) determining the activity of said polypeptide expressed in the host as defined in (a), which has not been contacted with said compound; and

   d) quantitatively relating the activity as determined in (b) and (c), wherein a decreased activity determined in (b) in comparison to (c) is indicative for an inhibitor or antagonist.

15. A screening method for identifying and/or obtaining a compound which is an inhibitor of the expression of a polypeptide listed in tables 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of

   a) contacting a host which expresses said polypeptide with a compound,

   b) determining the expression level and/or activity of said polypeptide;

   c) determining the expression level and/or activity of said polypeptide in the host as defined in (a), which has not been contacted with said compound; and

   d) quantitatively relating the expression level of said polypeptide as determined in (b) and (c), wherein a decreased expression level determined in (b) in comparison to (c) is indicative for an inhibitor of the expression of said polypeptide.

16. A compound identified and/or obtained by the screening methods of any one of claims 13 to 15.

17. A pharmaceutical composition comprising the compound of claim 16.

18.   A method for the preparation of the pharmaceutical composition of claim 17 comprising formulating the compound of claim 16 in a pharmaceutically acceptable carrier or diluent.

5   19.   Use of a compound of claim 16 for the preparation of a medicament for the treatment or prevention of pancreatic cancer.

20.   Use of a compound of claim 16 for the preparation of a diagnostic composition for diagnosing pancreatic cancer or a predisposition for pancreatic cancer.

10

21.   The use of claim 19 or 20 wherein said compound comprises an antibody, an antibody-derivative, an antibody fragment, a peptide or an antisense construct.

22.   Antibodies against the proteins listed in tables 2 and/or 3, or antigen-binding
15   fragments thereof, for the use in an in vitro method for the diagnosis of pancreatic cancer.

23.   A kit for the diagnosis of pancreatic cancer comprising one or more of the antibodies, or antigen-binding fragments thereof, of claim 22.

20

24.   A kit for the diagnosis of pancreatic cancer comprising one or more of the nucleic acids coding for the marker of claims 1 or 2.

25.   A kit for screening of compounds that activate or inhibit any of the polypeptides
25   listed in tables 2 and/or 3, or stimulate or inhibit the expression of any of said polypeptides.

26.   A marker for diagnosis of pancreatic cancer comprising at least one polypeptide selected from the group consisting of the polypeptides listed in table 6.

27.   The marker of claim 26, wherein said at least one polypeptide does not include Seq
5   ID No.s 25 and 50 to 55.

28.   The marker according to any one of claims 26 to 27, additionally comprising at least one of the polypeptides listed in table 5.

10   29.   An in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of

a) obtaining a biological sample; and

b) detecting and/or measuring the increase of at least one of the polypeptides listed in table 6.

15

30.   The in vitro method of claim 29, additionally comprising the step of detecting and/or measuring the decrease of at least one of the polypeptides listed in table 5.

31.   The in vitro method of claims 29 or 30, wherein said at least one polypeptide does
20   not include Seq ID No.s 25 and 50 to 55.

32.   The in vitro method of any one of claims 29 to 31, wherein said biological sample is derived from the group consisting of serum, plasma, pancreatic juice and cells of pancreatic tissue.

25

33.   An in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of

a) obtaining a biological sample; and

b) detecting and/or measuring the increase of at least one nucleic acid coding for the marker of any one of claims 26 to 28.

5   34.   The in vitro method of claim 33, wherein said nucleic acid molecule is RNA or DNA.

35.   The in vitro method of claim 34, wherein said DNA is a cDNA.

10   36.   The in vitro method of any one of claims 33 to 35, wherein the expression levels of at least one of said nucleic acids in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same nucleic acids in a healthy individual.

15   37.   The in vitro method of any one of claims 33 to 36, wherein the expression level of said marker in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same marker in a healthy individual.

20   38.   The in vitro method of claim 37, wherein an increase of the expression levels of said marker is indicative of pancreatic cancer or the susceptibility to pancreatic cancer.

39.   A screening method for identifying and/or obtaining a compound which interacts with a polypeptide selected from the group consisting of the polypeptides listed in table 6
25   whose expression is upregulated in pancreatic cancer, comprising the steps of

a) contacting said polypeptide with a compound or a plurality of compounds under conditions which allow interaction of said compound with said polypeptide; and

b) detecting the interaction between said compound or plurality of compounds with said polypeptide.

40.   A screening method for identifying and/or obtaining a compound which is an
5   inhibitor or an antagonist of a polypeptide listed in table 6 whose expression is upregulated in pancreatic cancer, comprising the steps of

a) contacting said polypeptide with a compound identified and/or obtained by the screening method of claim 39 under conditions which allow interaction of said compound with said polypeptide;

10   b) determining the activity of said polypeptide;

c) determining the activity of said polypeptide expressed in the host as defined in (a), which has not been contacted with said compound; and

d) quantitatively relating the activity as determined in (b) and (c), wherein a decreased activity determined in (b) in comparison to (c) is indicative for an
15   inhibitor or antagonist.

41.   A screening method for identifying and/or obtaining a compound which is an inhibitor of the expression of a polypeptide selected from the group consisting of the polypeptides listed in table 6 whose expression is upregulated in pancreatic cancer,
20   comprising the steps of

a) contacting a host which expresses said polypeptide with a compound,

b) determining the expression level and/or activity of said polypeptide;

c) determining the expression level and/or activity of said polypeptide in the host as defined in (a), which has not been contacted with said compound; and

25   d) quantitatively relating the expression level of said polypeptide as determined in (b) and (c), wherein a decreased expression level determined in (b) in comparison to (c) is indicative for an inhibitor of the expression of said polypeptide.

42. A compound identified and/or obtained by the screening methods of any one of claims 39 to 41.

43. A pharmaceutical composition comprising the compound of claim 42.

5

44. A method for the preparation of the pharmaceutical composition of claim 43 comprising formulating the compound of claim 42 in a pharmaceutically acceptable carrier or diluent.

10   45. Use of a compound of claim 42 for the preparation of a medicament for the treatment or prevention of pancreatic cancer.

46. Use of a compound of claim 42 for the preparation of a diagnostic composition for diagnosing pancreatic cancer or a predisposition for pancreatic cancer.

15

47. The use of claim 45 or 46 wherein said compound comprises an antibody, an antibody-derivative, an antibody fragment, a peptide or an antisense construct.

48. Antibodies against the proteins listed in tables 5 and/or 6, or antigen-binding
20   fragments thereof, for the use in an in vitro method for the diagnosis of pancreatic cancer.

49. A kit for the diagnosis of pancreatic cancer comprising one or more of the antibodies, or antigen-binding fragments thereof, of claim 48.

25

50. A kit for the diagnosis of pancreatic cancer comprising one or more of the nucleic acids coding for the marker of claims 26 to 28.

51.   A kit for screening of compounds that activate or inhibit any of the polypeptides
listed in table 5 and/or 6, or stimulate or inhibit the expression of any of said
polypeptides.

5

52.   The kit of claim 51, wherein said polypeptides are the polypeptides listed in table 6.

53.   The proteins, compounds, kits, methods and uses substantially as herein before
described, especially with reference to the foregoing examples.

10

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SEQUENCE LISTING

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Arg Arg Thr Met Ser Glu Val Gly Gly Ser Val Glu Asp Leu Ile Ala

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    Gly Pro Ile Pro Glu Val Leu Lys Asn Tyr Met Asp Ala Gln Tyr Tyr
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 5  Gly Glu Ile Gly Ile Gly Thr Pro Pro Gln Cys Phe Thr Val Val Phe
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    Asp Thr Gly Ser Ser Asn Leu Trp Val Pro Ser Ile His Cys Lys Leu
                        100                 105                 110

    Leu Asp Ile Ala Cys Trp Ile His His Lys Tyr Asn Ser Asp Lys Ser
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            130                 135                 140

    Gly Ser Leu Ser Gly Tyr Leu Ser Gln Asp Thr Val Ser Val Pro Cys
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15  Gln Ser Ala Ser Ser Ala Ser Ala Leu Gly Gly Val Lys Val Glu Arg
                        165                 170                 175

    Gln Val Phe Gly Glu Ala Thr Lys Gln Pro Gly Ile Thr Phe Ile Ala
                        180                 185                 190

    Ala Lys Phe Asp Gly Ile Leu Gly Met Ala Tyr Pro Arg Ile Ser Val
20          195                 200                 205

    Asn Asn Val Leu Pro Val Phe Asp Asn Leu Met Gln Gln Lys Leu Val
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    Asp Gln Asn Ile Phe Ser Phe Tyr Leu Ser Arg Asp Pro Asp Ala Gln
    225                 230                 235                 240
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     Pro Gly Gly Glu Leu Met Leu Gly Gly Thr Asp Ser Lys Tyr Tyr Lys
                      245              250              255

     Gly Ser Leu Ser Tyr Leu Asn Val Thr Arg Lys Ala Tyr Trp Gln Val
                      260              265              270

 5   His Leu Asp Gln Val Glu Val Ala Ser Gly Leu Thr Leu Cys Lys Glu
                      275              280              285

     Gly Cys Glu Ala Ile Val Asp Thr Gly Thr Ser Leu Met Val Gly Pro
                      290              295              300

     Val Asp Glu Val Arg Glu Leu Gln Lys Ala Ile Gly Ala Val Pro Leu
10   305              310              315              320

     Ile Gln Gly Glu Tyr Met Ile Pro Cys Glu Lys Val Ser Thr Leu Pro
                      325              330              335

     Ala Ile Thr Leu Lys Leu Gly Gly Lys Gly Tyr Lys Leu Ser Pro Glu
                      340              345              350

15   Asp Tyr Thr Leu Lys Val Ser Gln Ala Gly Lys Thr Leu Cys Leu Ser
                      355              360              365

     Gly Phe Met Gly Met Asp Ile Pro Pro Pro Ser Gly Pro Leu Trp Ile
                      370              375              380

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                          20                  25                  30

15    Pro Tyr Val Glu Leu Asp Leu His Ser Tyr Asp Leu Gly Ile Glu Asn

                  35                  40                  45

      Arg Asp Ala Thr Asn Asp Gln Val Thr Lys Asp Ala Ala Glu Ala Ile

              50                  55                  60

      Lys Lys His Asn Val Gly Val Lys Cys Ala Thr Ile Thr Pro Asp Glu

20    65                  70                  75                  80

      Lys Arg Val Glu Glu Phe Lys Leu Lys Gln Met Trp Lys Ser Pro Asn

                          85                  90                  95

      Gly Thr Ile Arg Asn Ile Leu Gly Gly Thr Val Phe Arg Glu Ala Ile

                      100                 105                 110
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5 Val Val Pro Gly Pro Gly Lys Val Glu Ile Thr Tyr Thr Pro Ser Asp

145   150   155   160

Gly Thr Gln Lys Val Thr Tyr Leu Val His Asn Phe Glu Glu Gly Gly

165   170   175

Gly Val Ala Met Gly Met Tyr Asn Gln Asp Lys Ser Ile Glu Asp Phe

10   180   185   190

Ala His Ser Ser Phe Gln Met Ala Leu Ser Lys Gly Trp Pro Leu Tyr

195   200   205

Leu Ser Thr Lys Asn Thr Ile Leu Lys Lys Tyr Asp Gly Arg Phe Lys

210   215   220

15 Asp Ile Phe Gln Glu Ile Tyr Asp Lys Gln Tyr Lys Ser Gln Phe Glu

225   230   235   240

Ala Gln Lys Ile Trp Tyr Glu His Arg Leu Ile Asp Asp Met Val Ala

245   250   255

Gln Ala Met Lys Ser Glu Gly Gly Phe Ile Trp Ala Cys Lys Asn Tyr

20   260   265   270

Asp Gly Asp Val Gln Ser Asp Ser Val Ala Gln Gly Tyr Gly Ser Leu

275   280   285

Gly Met Met Thr Ser Val Leu Val Cys Pro Asp Gly Lys Thr Val Glu

290   295   300

Ala Glu Ala Ala His Gly Thr Val Thr Arg His Tyr Arg Met Tyr Gln

305   310   315   320

Lys Gly Gln Glu Thr Ser Thr Asn Pro Ile Ala Ser Ile Phe Ala Trp

                325   330   335

5   Thr Arg Gly Leu Ala His Arg Ala Lys Leu Asp Asn Asn Lys Glu Leu

              340   345   350

Ala Phe Phe Ala Asn Ala Leu Glu Glu Val Ser Ile Glu Thr Ile Glu

              355   360   365

Ala Gly Phe Met Thr Lys Asp Leu Ala Ala Cys Ile Lys Gly Leu Pro

10   370   375   380

Asn Val Gln Arg Ser Asp Tyr Leu Asn Thr Phe Glu Phe Met Asp Lys

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Leu Gly Glu Asn Leu Lys Ile Lys Leu Ala Gln Ala Lys Leu

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                50                  55                  60

        Glu Pro Gly Leu Gln Ile Trp Arg Val Glu Lys Phe Asp Leu Val Pro
        65                  70                  75                  80

        Val Pro Thr Asn Leu Tyr Gly Asp Phe Phe Thr Gly Asp Ala Tyr Val
                        85                  90                  95

   15   Ile Leu Lys Thr Val Gln Leu Arg Asn Gly Asn Leu Gln Tyr Asp Leu
                        100                 105                 110

        His Tyr Trp Leu Gly Asn Glu Cys Ser Gln Asp Glu Ser Gly Ala Ala
                        115                 120                 125

        Ala Ile Phe Thr Val Gln Leu Asp Asp Tyr Leu Asn Gly Arg Ala Val
   20           130                 135                 140

        Gln His Arg Glu Val Gln Gly Phe Glu Ser Ala Thr Phe Leu Gly Tyr
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                       210   215   220

      His Gln Trp Cys Gly Ser Asn Ser Asn Arg Tyr Glu Arg Leu Lys Ala

      225   230   235   240

      Thr Gln Val Ser Lys Gly Ile Arg Asp Asn Glu Arg Ser Gly Arg Ala

10   245   250   255

      Arg Val His Val Ser Glu Glu Gly Thr Glu Pro Glu Ala Met Leu Gln

                       260   265   270

      Val Leu Gly Pro Lys Pro Ala Leu Pro Ala Gly Thr Glu Asp Thr Ala

                       275   280   285

15   Lys Glu Asp Ala Ala Asn Arg Lys Leu Ala Lys Leu Tyr Lys Val Ser

                       290   295   300

      Asn Gly Ala Gly Thr Met Ser Val Ser Leu Val Ala Asp Glu Asn Pro

      305   310   315   320

      Phe Ala Gln Gly Ala Leu Lys Ser Glu Asp Cys Phe Ile Leu Asp His

20   325   330   335

      Gly Lys Asp Gly Lys Ile Phe Val Trp Lys Gly Lys Gln Ala Asn Thr

                       340   345   350

      Glu Glu Arg Lys Ala Ala Leu Lys Thr Ala Ser Asp Phe Ile Thr Lys

                      355   360   365

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 5   Gln Thr Asp Gly Leu Gly Leu Ser Tyr Leu Ser Ser His Ile Ala Asn

                         405             410             415

     Val Glu Arg Val Pro Phe Asp Ala Ala Thr Leu His Thr Ser Thr Ala

                 420             425             430

     Met Ala Ala Gln His Gly Met Asp Asp Asp Gly Thr Gly Gln Lys Gln

10           435             440             445

     Ile Trp Arg Ile Glu Gly Ser Asn Lys Val Pro Val Asp Pro Ala Thr

             450             455             460

     Tyr Gly Gln Phe Tyr Gly Gly Asp Ser Tyr Ile Ile Leu Tyr Asn Tyr

         465             470             475             480

15   Arg His Gly Gly Arg Gln Gly Gln Ile Ile Tyr Asn Trp Gln Gly Ala

                         485             490             495

     Gln Ser Thr Gln Asp Glu Val Ala Ala Ser Ala Ile Leu Thr Ala Gln

                 500             505             510

     Leu Asp Glu Glu Leu Gly Gly Thr Pro Val Gln Ser Arg Val Val Gln

20           515             520             525

     Gly Lys Glu Pro Ala His Leu Met Ser Leu Phe Gly Gly Lys Pro Met

             530             535             540

     Ile Ile Tyr Lys Gly Gly Thr Ser Arg Glu Gly Gly Gln Thr Ala Pro

         545             550             555             560
```

Ala Ser Thr Arg Leu Phe Gln Val Arg Ala Asn Ser Ala Gly Ala Thr

565   570   575

Arg Ala Val Glu Val Leu Pro Lys Ala Gly Ala Leu Asn Ser Asn Asp

580   585   590

5   Ala Phe Val Leu Lys Thr Pro Ser Ala Ala Tyr Leu Trp Val Gly Thr

595   600   605

Gly Ala Ser Glu Ala Glu Lys Thr Gly Ala Gln Glu Leu Leu Arg Val

610   615   620

Leu Arg Ala Gln Pro Val Gln Val Ala Glu Gly Ser Glu Pro Asp Gly

10 625   630   635   640

Phe Trp Glu Ala Leu Gly Gly Lys Ala Ala Tyr Arg Thr Ser Pro Arg

645   650   655

Leu Lys Asp Lys Lys Met Asp Ala His Pro Pro Arg Leu Phe Ala Cys

660   665   670

15 Ser Asn Lys Ile Gly Arg Phe Val Ile Glu Glu Val Pro Gly Glu Leu

675   680   685

Met Gln Glu Asp Leu Ala Thr Asp Asp Val Met Leu Leu Asp Thr Trp

690   695   700

Asp Gln Val Phe Val Trp Val Gly Lys Asp Ser Gln Glu Glu Glu Lys

20 705   710   715   720

Thr Glu Ala Leu Thr Ser Ala Lys Arg Tyr Ile Glu Thr Asp Pro Ala

725   730   735

Asn Arg Asp Arg Arg Thr Pro Ile Thr Val Val Lys Gln Gly Phe Glu

740   745   750

```
Pro Pro Ser Phe Val Gly Trp Phe Leu Gly Trp Asp Asp Asp Tyr Trp
        755                 760                 765

Ser Val Asp Pro Leu Asp Arg Ala Met Ala Glu Leu Ala Ala
        770                 775                 780
```

5

<210> 4

<211> 764

<212> PRT

10   <213> Homo sapiens

<220>

<221> Complement factor B precursor

<222> (1)..(764)

<223> Accession No. as of 06 Dec 2002: P00751

15   <400> 4


```
Met Gly Ser Asn Leu Ser Pro Gln Leu Cys Leu Met Pro Phe Ile Leu
1               5                   10                  15

Gly Leu Leu Ser Gly Gly Val Thr Thr Thr Pro Trp Ser Leu Ala Arg
20              20                  25                  30

Pro Gln Gly Ser Cys Ser Leu Glu Gly Val Glu Ile Lys Gly Gly Ser
                35                  40                  45

Phe Arg Leu Leu Gln Glu Gly Gln Ala Leu Glu Tyr Val Cys Pro Ser
        50                  55                  60
```

```
      Gly Phe Tyr Pro Tyr Pro Val Gln Thr Arg Thr Cys Arg Ser Thr Gly
      65                  70                  75                  80

      Ser Trp Ser Thr Leu Lys Thr Gln Asp Gln Lys Thr Val Arg Lys Ala
                          85                  90                  95

   5  Glu Cys Arg Ala Ile His Cys Pro Arg Pro His Asp Phe Glu Asn Gly
                      100                 105                 110

      Glu Tyr Trp Pro Arg Ser Pro Tyr Tyr Asn Val Ser Asp Glu Ile Ser
                      115                 120                 125

      Phe His Cys Tyr Asp Gly Tyr Thr Leu Arg Gly Ser Ala Asn Arg Thr
  10          130                 135                 140

      Cys Gln Val Asn Gly Arg Trp Ser Gly Gln Thr Ala Ile Cys Asp Asn
      145                 150                 155                 160

      Gly Ala Gly Tyr Cys Ser Asn Pro Gly Ile Pro Ile Gly Thr Arg Lys
                      165                 170                 175

  15  Val Gly Ser Gln Tyr Arg Leu Glu Asp Ser Val Thr Tyr His Cys Ser
                      180                 185                 190

      Arg Gly Leu Thr Leu Arg Gly Ser Gln Arg Arg Thr Cys Gln Glu Gly
                      195                 200                 205

      Gly Ser Trp Ser Gly Thr Glu Pro Ser Cys Gln Asp Ser Phe Met Tyr
  20          210                 215                 220

      Asp Thr Pro Gln Glu Val Ala Glu Ala Phe Leu Ser Ser Leu Thr Glu
      225                 230                 235                 240

      Thr Ile Glu Gly Val Asp Ala Glu Asp Gly His Gly Pro Gly Glu Gln
                      245                 250                 255
```

Gln Lys Arg Lys Ile Val Leu Asp Pro Ser Gly Ser Met Asn Ile Tyr
            260   265   270

Leu Val Leu Asp Gly Ser Asp Ser Ile Gly Ala Ser Asn Phe Thr Gly
            275   280   285

5 Ala Lys Lys Cys Leu Val Asn Leu Ile Glu Lys Val Ala Ser Tyr Gly
            290   295   300

Val Lys Pro Arg Tyr Gly Leu Val Thr Tyr Ala Thr Tyr Pro Lys Ile
305   310   315   320

Trp Val Lys Val Ser Glu Ala Asp Ser Ser Asn Ala Asp Trp Val Thr
10   325   330   335

Lys Gln Leu Asn Glu Ile Asn Tyr Glu Asp His Lys Leu Lys Ser Gly
                340   345   350

Thr Asn Thr Lys Lys Ala Leu Gln Ala Val Tyr Ser Met Met Ser Trp
                355   360   365

15 Pro Asp Asp Val Pro Pro Glu Gly Trp Asn Arg Thr Arg His Val Ile
                370   375   380

Ile Leu Met Thr Asp Gly Leu His Asn Met Gly Gly Asp Pro Ile Thr
385   390   395   400

Val Ile Asp Glu Ile Arg Asp Leu Leu Tyr Ile Gly Lys Asp Arg Lys
20   405   410   415

Asn Pro Arg Glu Asp Tyr Leu Asp Val Tyr Val Phe Gly Val Gly Pro
                420   425   430

Leu Val Asn Gln Val Asn Ile Asn Ala Leu Ala Ser Lys Lys Asp Asn
                435   440   445

```
     Glu Gln His Val Phe Lys Val Lys Asp Met Glu Asn Leu Glu Asp Val
            450             455             460

     Phe Tyr Gln Met Ile Asp Glu Ser Gln Ser Leu Ser Leu Cys Gly Met
     465             470             475             480

   5 Val Trp Glu His Arg Lys Gly Thr Asp Tyr His Lys Gln Pro Trp Gln
                    485             490             495

     Ala Lys Ile Ser Val Ile Arg Pro Ser Lys Gly His Glu Ser Cys Met
                    500             505             510

     Gly Ala Val Val Ser Glu Tyr Phe Val Leu Thr Ala Ala His Cys Phe
  10          515             520             525

     Thr Val Asp Asp Lys Glu His Ser Ile Lys Val Ser Val Gly Gly Glu
             530             535             540

     Lys Arg Asp Leu Glu Ile Glu Val Val Leu Phe His Pro Asn Tyr Asn
     545             550             555             560

  15 Ile Asn Gly Lys Lys Glu Ala Gly Ile Pro Glu Phe Tyr Asp Tyr Asp
                    565             570             575

     Val Ala Leu Ile Lys Leu Lys Asn Lys Leu Lys Tyr Gly Gln Thr Ile
                    580             585             590

     Arg Pro Ile Cys Leu Pro Cys Thr Glu Gly Thr Thr Arg Ala Leu Arg
  20          595             600             605

     Leu Pro Pro Thr Thr Thr Cys Gln Gln Gln Lys Glu Glu Leu Leu Pro
             610             615             620

     Ala Gln Asp Ile Lys Ala Leu Phe Val Ser Glu Glu Glu Lys Lys Leu
     625             630             635             640
```

Thr Arg Lys Glu Val Tyr Ile Lys Asn Gly Asp Lys Lys Gly Ser Cys

                  645   650   655

Glu Arg Asp Ala Gln Tyr Ala Pro Gly Tyr Asp Lys Val Lys Asp Ile

                  660   665   670

5 Ser Glu Val Val Thr Pro Arg Phe Leu Cys Thr Gly Gly Val Ser Pro

                  675   680   685

Tyr Ala Asp Pro Asn Thr Cys Arg Gly Asp Ser Gly Gly Pro Leu Ile

                  690   695   700

Val His Lys Arg Ser Arg Phe Ile Gln Val Gly Val Ile Ser Trp Gly

10 705   710   715   720

Val Val Asp Val Cys Lys Asn Gln Lys Arg Gln Lys Gln Val Pro Ala

                  725   730   735

His Ala Arg Asp Phe His Ile Asn Leu Phe Gln Val Leu Pro Trp Leu

                  740   745   750

15 Lys Glu Lys Leu Gln Asp Glu Asp Leu Gly Phe Leu

                  755   760

<210> 5

20 <211> 911

    <212> PRT

    <213> Homo sapiens

    <220>

    <221> Alpha-actinin 4

<222>   (1)..(911)

<223>   Accession No. O43707

<400>   5

5   Met Val Asp Tyr His Ala Ala Asn Gln Ser Tyr Gln Tyr Gly Pro Ser

     1   5   10   15

     Ser Ala Gly Asn Gly Ala Gly Gly Gly Ser Met Gly Asp Tyr Met

                     20   25   30

     Ala Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp

10   35   40   45

     Glu Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu

                 50   55   60

     Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp Glu Asp Phe Arg Asp

                 65   70   75   80

15   Gly Leu Lys Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu

                         85   90   95

     Pro Lys Pro Glu Arg Gly Lys Met Arg Val His Lys Ile Asn Asn Val

                     100   105   110

     Asn Lys Ala Leu Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser

20   115   120   125

     Ile Gly Ala Glu Glu Ile Val Asp Gly Asn Ala Lys Met Thr Leu Gly

                 130   135   140

     Met Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val

     145   150   155   160

Glu Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys
              165   170   175

Thr Ala Pro Tyr Lys Asn Val Asn Val Gln Asn Phe His Ile Ser Trp
              180   185   190

5 Lys Asp Gly Leu Ala Phe Asn Ala Leu Ile His Arg His Arg Pro Glu
              195   200   205

Leu Ile Glu Tyr Asp Lys Leu Arg Lys Asp Asp Pro Val Thr Asn Leu
              210   215   220

Asn Asn Ala Phe Glu Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met
10 225   230   235   240

Leu Asp Ala Glu Asp Ile Val Asn Thr Ala Arg Pro Asp Glu Lys Ala
              245   250   255

Ile Met Thr Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln
              260   265   270

15 Lys Ala Glu Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val Asn
              275   280   285

Gln Glu Asn Glu His Leu Met Glu Asp Tyr Glu Lys Leu Ala Ser Asp
              290   295   300

Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asp Arg Val
20 305   310   315   320

Pro Gln Lys Thr Ile Gln Glu Met Gln Gln Lys Leu Glu Asp Phe Arg
              325   330   335

Asp Tyr Arg Arg Val His Lys Pro Pro Lys Val Gln Glu Lys Cys Gln
              340   345   350

Leu Glu Ile Asn Phe Asn Thr Leu Gln Thr Lys Leu Arg Leu Ser Asn

        355   360   365

Arg Pro Ala Phe Met Pro Ser Glu Gly Lys Met Val Ser Asp Ile Asn

        370   375   380

5   Asn Gly Trp Gln His Leu Glu Gln Ala Glu Lys Gly Tyr Glu Glu Trp

    385   390   395   400

Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu Ala Glu

            405   410   415

Lys Phe Arg Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp Gly Lys

10   420   425   430

Glu Ala Met Leu Lys His Arg Asp Tyr Glu Thr Ala Thr Leu Ser Asp

        435   440   445

Ile Lys Ala Leu Ile Arg Lys His Glu Ala Phe Glu Ser Asp Leu Ala

        450   455   460

15   Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ile Ala Gln Glu Leu

  465   470   475   480

Asn Glu Leu Asp Tyr Tyr Asp Ser His Asn Val Asn Thr Arg Cys Gln

            485   490   495

Lys Ile Cys Asp Gln Trp Asp Ala Leu Gly Ser Leu Thr His Ser Arg

20   500   505   510

Arg Glu Ala Leu Glu Lys Thr Glu Lys Gln Leu Glu Ala Ile Asp Gln

        515   520   525

Leu His Leu Glu Tyr Ala Lys Arg Ala Ala Pro Phe Asn Asn Trp Met

        530   535   540

Glu Ser Ala Met Glu Asp Leu Gln Asp Met Phe Ile Val His Thr Ile

545   550   555   560

Glu Glu Ile Glu Gly Leu Ile Ser Ala His Asp Gln Phe Lys Ser Thr

              565   570   575

5   Leu Pro Asp Ala Asp Arg Glu Arg Glu Ala Ile Leu Ala Ile His Lys

              580   585   590

Glu Ala Gln Arg Ile Ala Glu Ser Asn His Ile Lys Leu Ser Gly Ser

              595   600   605

Asn Pro Tyr Thr Thr Val Thr Pro Gln Ile Ile Asn Ser Lys Trp Glu

10   610   615   620

Lys Val Gln Gln Leu Val Pro Lys Arg Asp His Ala Leu Leu Glu Glu

625   630   635   640

Gln Ser Lys Gln Gln Ser Asn Glu His Leu Arg Arg Gln Phe Ala Ser

              645   650   655

15 Gln Ala Asn Val Val Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile

              660   665   670

Gly Arg Ile Ser Ile Glu Met Asn Gly Thr Leu Glu Asp Gln Leu Ser

              675   680   685

His Leu Lys Gln Tyr Glu Arg Ser Ile Val Asp Tyr Lys Pro Asn Leu

20   690   695   700

Asp Leu Leu Glu Gln Gln His Gln Leu Ile Gln Glu Ala Leu Ile Phe

705   710   715   720

Asp Asn Lys His Thr Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp

              725   730   735

Glu Gln Leu Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val Glu Asn
             740   745   750

Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln Met Gln
             755   760   765

5 Glu Phe Arg Ala Ser Phe Asn His Phe Asp Lys Asp His Gly Gly Ala
             770   775   780

Leu Gly Pro Glu Glu Phe Lys Ala Cys Leu Ile Ser Leu Gly Tyr Asp
785   790   795   800

Val Glu Asn Asp Arg Gln Gly Glu Ala Glu Phe Asn Arg Ile Met Ser
10   805   810   815

Leu Val Asp Pro Asn His Ser Gly Leu Val Thr Phe Gln Ala Phe Ile
             820   825   830

Asp Phe Met Ser Arg Glu Thr Thr Asp Thr Asp Thr Ala Asp Gln Val
             835   840   845

15 Ile Ala Ser Phe Lys Val Leu Ala Gly Asp Lys Asn Phe Ile Thr Ala
             850   855   860

Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln Ala Glu Tyr Cys Ile
865   870   875   880

Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp Ala Val Pro Gly Ala Leu
20   885   890   895

Asp Tyr Lys Ser Phe Ser Thr Ala Leu Tyr Gly Glu Ser Asp Leu
             900   905   910

```
    <210>   6

    <211>   683

    <212>   PRT

    <213>   Homo sapiens

5   <220>

    <221>   Transforming growth factor-beta induced protein IG-H3 precursor

    <222>   (1)..(683)

    <223>   Accession No. as of 06 Dec 2002: Q15582

    <400>   6

10
```

```
    Met Ala Leu Phe Val Arg Leu Leu Ala Leu Ala Leu Ala Leu Ala Leu

    1               5                   10                  15

    Gly Pro Ala Ala Thr Leu Ala Gly Pro Ala Lys Ser Pro Tyr Gln Leu

                    20                  25                  30

15  Val Leu Gln His Ser Arg Leu Arg Gly Arg Gln His Gly Pro Asn Val

                    35                  40                  45

    Cys Ala Val Gln Lys Val Ile Gly Thr Asn Arg Lys Tyr Phe Thr Asn

                50                  55                  60

    Cys Lys Gln Trp Tyr Gln Arg Lys Ile Cys Gly Lys Ser Thr Val Ile

20  65                  70                  75                  80

    Ser Tyr Glu Cys Cys Pro Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly

                    85                  90                  95

    Cys Pro Ala Ala Leu Pro Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val

                    100                 105                 110
```

Val Gly Ser Thr Thr Thr Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu

     115   120   125

Arg Pro Glu Met Glu Gly Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser

     130   135   140

5   Asn Glu Ala Trp Ala Ser Leu Pro Ala Glu Val Leu Asp Ser Leu Val

     145   150   155   160

Ser Asn Val Asn Ile Glu Leu Leu Asn Ala Leu Arg Tyr His Met Val

           165   170   175

Gly Arg Arg Val Leu Thr Asp Glu Leu Lys His Gly Met Thr Leu Thr

10   180   185   190

Ser Met Tyr Gln Asn Ser Asn Ile Gln Ile His His Tyr Pro Asn Gly

          195   200   205

Ile Val Thr Val Asn Cys Ala Arg Leu Leu Lys Ala Asp His His Ala

     210   215   220

15 Thr Asn Gly Val Val His Leu Ile Asp Lys Val Ile Ser Thr Ile Thr

     225   230   235   240

Asn Asn Ile Gln Gln Ile Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu

          245   250   255

Arg Ala Ala Val Ala Ala Ser Gly Leu Asn Thr Met Leu Glu Gly Asn

20   260   265   270

Gly Gln Tyr Thr Leu Leu Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile

          275   280   285

Pro Ser Glu Thr Leu Asn Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg

     290   295   300

Asp Leu Leu Asn Asn His Ile Leu Lys Ser Ala Met Cys Ala Glu Ala
305   310   315   320

Ile Val Ala Gly Leu Ser Val Glu Thr Leu Glu Gly Thr Thr Leu Glu
325   330   335

5   Val Gly Cys Ser Gly Asp Met Leu Thr Ile Asn Gly Lys Ala Ile Ile
340   345   350

Ser Asn Lys Asp Ile Leu Ala Thr Asn Gly Val Ile His Tyr Ile Asp
355   360   365

Glu Leu Leu Ile Pro Asp Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala
10   370   375   380

Glu Ser Asp Val Ser Thr Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu
385   390   395   400

Gly Asn His Leu Ser Gly Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu
405   410   415

15 Asn Ser Val Phe Lys Asp Gly Thr Pro Pro Ile Asp Ala His Thr Arg
420   425   430

Asn Leu Leu Arg Asn His Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr
435   440   445

Leu Tyr His Gly Gln Thr Leu Glu Thr Leu Gly Gly Lys Lys Leu Arg
20   450   455   460

Val Phe Val Tyr Arg Asn Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala
465   470   475   480

Ala His Asp Lys Arg Gly Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg
485   490   495

Val Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp
                    500   505   510

Asn Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr
                    515   520   525

5   Glu Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn
                    530   535   540

Glu Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly
545   550   555   560

Asp Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu
10   565   570   575

Ile Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu
                    580   585   590

Gln Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val
                    595   600   605

15   Asn Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val
                    610   615   620

Val His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Arg Pro Gln
625   630   635   640

Glu Arg Gly Asp Glu Leu Ala Asp Ser Ala Leu Glu Ile Phe Lys Gln
20   645   650   655

Ala Ser Ala Phe Ser Arg Ala Ser Gln Arg Ser Val Arg Leu Ala Pro
                    660   665   670

Val Tyr Gln Lys Leu Leu Glu Arg Met Lys His
                    675   680

```
     Met Asp His Tyr Asp Ser Gln Gln Thr Asn Asp Tyr Met Gln Pro Glu

     1               5                   10                  15

15   Glu Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp Glu Lys Gln

                     20                  25                  30

     Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu Arg Lys Ala

                     35                  40                  45

     Gly Thr Gln Ile Glu Asn Ile Glu Glu Asp Phe Arg Asp Gly Leu Lys

20        50                  55                  60

     Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Ala Lys Pro

     65                  70                  75                  80

     Glu Arg Gly Lys Met Arg Val His Lys Ile Ser Asn Val Asn Lys Ala

                     85                  90                  95
```

```
      Leu Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser Ile Gly Ala
                      100               105               110

      Glu Glu Ile Val Asp Gly Asn Val Lys Met Thr Leu Gly Met Ile Trp
                      115               120               125

   5  Thr Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val Glu Glu Thr
                      130               135               140

      Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys Thr Ala Pro
         145               150               155               160

      Tyr Lys Asn Val Asn Ile Gln Asn Phe His Ile Ser Trp Lys Asp Gly
  10                    165               170               175

      Leu Gly Phe Cys Ala Leu Ile His Arg His Arg Pro Glu Leu Ile Asp
                      180               185               190

      Tyr Gly Lys Leu Arg Lys Asp Asp Pro Leu Thr Asn Leu Asn Thr Ala
                      195               200               205

  15  Phe Asp Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met Leu Asp Ala
                      210               215               220

      Glu Asp Ile Val Gly Thr Ala Arg Pro Asp Glu Lys Ala Ile Met Thr
         225               230               235               240

      Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln Lys Ala Glu
  20                    245               250               255

      Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val Asn Gln Glu Asn
                      260               265               270

      Glu Gln Leu Met Glu Asp Tyr Glu Lys Leu Ala Ser Asp Leu Leu Glu
                      275               280               285
```

Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asn Arg Val Pro Glu Asn
     290   295   300

Thr Met His Ala Met Gln Gln Lys Leu Glu Asp Phe Arg Asp Tyr Arg
     305   310   315   320

5   Arg Leu His Lys Pro Pro Lys Val Gln Glu Lys Cys Gln Leu Glu Ile
                     325   330   335

Asn Phe Asn Thr Leu Gln Thr Lys Leu Arg Leu Ser Asn Arg Pro Ala
                 340   345   350

Phe Met Pro Ser Glu Gly Arg Met Val Ser Asp Ile Asn Asn Ala Trp
10   355   360   365

Gly Cys Leu Glu Gln Val Glu Lys Gly Tyr Glu Glu Trp Leu Leu Asn
                 370   375   380

Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu Ala Glu Lys Phe Arg
     385   390   395   400

15   Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp Gly Lys Glu Ala Met
                     405   410   415

Leu Arg Gln Lys Asp Tyr Glu Thr Ala Thr Leu Ser Glu Ile Lys Ala
                 420   425   430

Leu Leu Lys Lys His Glu Ala Phe Glu Ser Asp Leu Ala Ala His Gln
20   435   440   445

Asp Arg Val Glu Gln Ile Ala Ala Ile Ala Gln Glu Leu Asn Glu Leu
                 450   455   460

Asp Tyr Tyr Asp Ser Pro Ser Val Asn Ala Arg Cys Gln Lys Ile Cys
     465   470   475   480

Asp Gln Trp Asp Asn Leu Gly Ala Leu Thr Gln Lys Arg Arg Glu Ala

                485   490   495

Leu Glu Arg Thr Glu Lys Leu Leu Glu Thr Ile Asp Gln Leu Tyr Leu

                500   505   510

 5 Glu Tyr Ala Lys Arg Ala Ala Pro Phe Asn Asn Trp Met Glu Gly Ala

                515   520   525

Met Glu Asp Leu Gln Asp Thr Phe Ile Val His Thr Ile Glu Glu Ile

                530   535   540

Gln Gly Leu Thr Thr Ala His Glu Gln Phe Lys Ala Thr Leu Pro Asp

10 545   550   555   560

Ala Asp Lys Glu Arg Leu Ala Ile Leu Gly Ile His Asn Glu Val Ser

                565   570   575

Lys Ile Val Gln Thr Tyr His Val Asn Met Ala Gly Thr Asn Pro Tyr

                580   585   590

15 Thr Thr Ile Thr Pro Gln Glu Ile Asn Gly Lys Trp Asp His Val Arg

                595   600   605

Gln Leu Val Pro Arg Arg Asp Gln Ala Leu Thr Glu Glu His Ala Arg

                610   615   620

Gln Gln His Asn Glu Ser Val Arg Lys Gln Phe Gly Ala Gln Ala Asn

20 625   630   635   640

Val Ile Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile Gly Arg Ile

                645   650   655

Ser Ile Glu Met His Gly Thr Leu Glu Asp Gln Leu Ser His Leu Arg

                660   665   670

Gln Tyr Glu Lys Ser Ile Val Asn Tyr Lys Pro Lys Ile Asp Gln Leu

675   680   685

Glu Gly Asp His Gln Leu Ile Gln Glu Ala Leu Ile Phe Asp Asn Lys

690   695   700

5   His Thr Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp Glu Gln Leu

705   710   715   720

Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val Glu Asn Gln Ile Leu

725   730   735

Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln Met Asn Glu Phe Arg

10   740   745   750

Ala Ser Phe Asn His Phe Asp Arg Asp His Ser Gly Thr Leu Gly Pro

755   760   765

Glu Glu Phe Lys Ala Cys Leu Ile Ser Leu Gly Tyr Asp Ile Gly Asn

770   775   780

15 Asp Pro Gln Gly Glu Ala Glu Phe Ala Arg Ile Met Ser Ile Val Asp

785   790   795   800

Pro Asn Arg Leu Gly Val Val Thr Phe Gln Ala Phe Ile Asp Phe Met

805   810   815

Ser Arg Glu Thr Ala Asp Thr Asp Thr Ala Asp Gln Val Met Ala Ser

20   820   825   830

Phe Lys Ile Leu Ala Gly Asp Lys Asn Tyr Ile Thr Met Asp Glu Leu

835   840   845

Arg Arg Glu Leu Pro Pro Asp Gln Ala Glu Tyr Cys Ile Ala Arg Met

850   855   860

```
Ala Pro Tyr Thr Gly Pro Asp Ser Val Pro Gly Ala Leu Asp Tyr Met

    865             870             875             880

Ser Phe Ser Thr Ala Leu Tyr Gly Glu Ser Asp Leu

                885             890
```

5


```
<210>   8

<211>   448

<212>   PRT

10   <213>   Homo sapiens

<220>

<221>   Tubulin alpha-4 chain

<222>   (1)..(448)

<223>   Accession No. P05215

15   <400>   8
```


```
Met Arg Glu Cys Ile Ser Val His Val Gly Gln Ala Gly Val Gln Met

1               5               10              15

Gly Asn Ala Cys Trp Glu Leu Tyr Cys Leu Glu His Gly Ile Gln Pro

20              20              25              30

Asp Gly Gln Met Pro Ser Asp Lys Thr Ile Gly Gly Gly Asp Asp Ser

                35              40              45

Phe Thr Thr Phe Phe Cys Glu Thr Gly Ala Gly Lys His Val Pro Arg

            50              55              60
```

```
   Ala Val Phe Val Asp Leu Glu Pro Thr Val Ile Asp Glu Ile Arg Asn

   65                  70                  75                  80

   Gly Pro Tyr Arg Gln Leu Phe His Pro Glu Gln Leu Ile Thr Gly Lys

                      85                  90                  95

 5 Glu Asp Ala Ala Asn Asn Tyr Ala Arg Gly His Tyr Thr Ile Gly Lys

                     100                 105                 110

   Glu Ile Ile Asp Pro Val Leu Asp Arg Ile Arg Lys Leu Ser Asp Gln

                 115                 120                 125

   Cys Thr Gly Leu Gln Gly Phe Leu Val Phe His Ser Phe Gly Gly Gly

10       130                 135                 140

   Thr Gly Ser Gly Phe Thr Ser Leu Leu Met Glu Arg Leu Ser Val Asp

   145                 150                 155                 160

   Tyr Gly Lys Lys Ser Lys Leu Glu Phe Ser Ile Tyr Pro Ala Pro Gln

                     165                 170                 175

15 Val Ser Thr Ala Val Val Glu Pro Tyr Asn Ser Ile Leu Thr Thr His

                 180                 185                 190

   Thr Thr Leu Glu His Ser Asp Cys Ala Phe Met Val Asp Asn Glu Ala

             195                 200                 205

   Ile Tyr Asp Ile Cys Arg Arg Asn Leu Asp Ile Glu Arg Pro Thr Tyr

20       210                 215                 220

   Thr Asn Leu Asn Arg Leu Ile Ser Gln Ile Val Ser Ser Ile Thr Ala

   225                 230                 235                 240

   Ser Leu Arg Phe Asp Gly Ala Leu Asn Val Asp Leu Thr Glu Phe Gln

                     245                 250                 255
```

```
     Thr Asn Leu Val Pro Tyr Pro Arg Ile His Phe Pro Leu Ala Thr Tyr
                     260                 265                 270

     Ala Pro Val Ile Ser Ala Glu Lys Ala Tyr His Glu Gln Leu Ser Val
                     275                 280                 285

 5   Ala Glu Ile Thr Asn Ala Cys Phe Glu Pro Ala Asn Gln Met Val Lys
                     290                 295                 300

     Cys Asp Pro Arg His Gly Lys Tyr Met Ala Cys Cys Leu Leu Tyr Arg
     305                 310                 315                 320

     Gly Asp Val Val Pro Lys Asp Val Asn Ala Ala Ile Ala Ala Ile Lys
 10                      325                 330                 335

     Thr Lys Arg Ser Ile Gln Phe Val Asp Trp Cys Pro Thr Gly Phe Lys
                     340                 345                 350

     Val Gly Ile Asn Tyr Gln Pro Pro Thr Val Val Pro Gly Gly Asp Leu
                     355                 360                 365

 15  Ala Lys Val Gln Arg Ala Val Cys Met Leu Ser Asn Thr Thr Ala Ile
                     370                 375                 380

     Ala Glu Ala Trp Ala Arg Leu Asp His Lys Phe Asp Leu Met Tyr Ala
     385                 390                 395                 400

     Lys Arg Ala Phe Val His Trp Tyr Val Gly Glu Gly Met Glu Glu Gly
 20                      405                 410                 415

     Glu Phe Ser Glu Ala Arg Glu Asp Met Ala Ala Leu Glu Lys Asp Tyr
                     420                 425                 430

     Glu Glu Val Gly Ile Asp Ser Tyr Glu Asp Glu Asp Glu Gly Glu Glu
                     435                 440                 445
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<210> 9

<211> 2647

5 <212> PRT

<213> Homo sapiens

<220>

<221> Filamin A

<222> (1)..(2647)

10 <223> Accession No. P21333

<400> 9

Met Ser Ser Ser His Ser Arg Ala Gly Gln Ser Ala Ala Gly Ala Ala

1   5   10   15

15 Pro Gly Gly Gly Val Asp Thr Arg Asp Ala Glu Met Pro Ala Thr Glu

               20   25   30

Lys Asp Leu Ala Glu Asp Ala Pro Trp Lys Lys Ile Gln Gln Asn Thr

            35   40   45

Phe Thr Arg Trp Cys Asn Glu His Leu Lys Cys Val Ser Lys Arg Ile

20   50   55   60

Ala Asn Leu Gln Thr Asp Leu Ser Asp Gly Leu Arg Leu Ile Ala Leu

    65   70   75   80

Leu Glu Val Leu Ser Gln Lys Lys Met His Arg Lys His Asn Gln Arg

                85   90   95

Pro Thr Phe Arg Gln Met Gln Leu Glu Asn Val Ser Val Ala Leu Glu

100   105   110

Phe Leu Asp Arg Glu Ser Ile Lys Leu Val Ser Ile Asp Ser Lys Ala

115   120   125

5   Ile Val Asp Gly Asn Leu Lys Leu Ile Leu Gly Leu Ile Trp Thr Leu

130   135   140

Ile Leu His Tyr Ser Ile Ser Met Pro Met Trp Asp Glu Glu Glu Asp

145   150   155   160

Glu Glu Ala Lys Lys Gln Thr Pro Lys Gln Arg Leu Leu Gly Trp Ile

10   165   170   175

Gln Asn Lys Leu Pro Gln Leu Pro Ile Thr Asn Phe Ser Arg Asp Trp

180   185   190

Gln Ser Gly Arg Ala Leu Gly Ala Leu Val Asp Ser Cys Ala Pro Gly

195   200   205

15 Leu Cys Pro Asp Trp Asp Ser Trp Asp Ala Ser Lys Pro Val Thr Asn

210   215   220

Ala Arg Glu Ala Met Gln Gln Ala Asp Asp Trp Leu Gly Ile Pro Gln

225   230   235   240

Val Ile Thr Pro Glu Glu Ile Val Asp Pro Asn Val Asp Glu His Ser

20   245   250   255

Val Met Thr Tyr Leu Ser Gln Phe Pro Lys Ala Lys Leu Lys Pro Gly

260   265   270

Ala Pro Leu Arg Pro Lys Leu Asn Pro Lys Lys Ala Arg Ala Tyr Gly

275   280   285

```
     Pro Gly Ile Glu Pro Thr Gly Asn Met Val Lys Lys Arg Ala Glu Phe
              290             295             300

     Thr Val Glu Thr Arg Ser Ala Gly Gln Gly Glu Val Leu Val Tyr Val
     305             310             315             320

 5   Glu Asp Pro Ala Gly His Gln Glu Glu Ala Lys Val Thr Ala Asn Asn
                     325             330             335

     Asp Lys Asn Arg Thr Phe Ser Val Trp Tyr Val Pro Glu Val Thr Gly
                 340             345             350

     Thr His Lys Val Thr Val Leu Phe Ala Gly Gln His Ile Ala Lys Ser
10               355             360             365

     Pro Phe Glu Val Tyr Val Asp Lys Ser Gln Gly Asp Ala Ser Lys Val
                 370             375             380

     Thr Ala Gln Gly Pro Gly Leu Glu Pro Ser Gly Asn Ile Ala Asn Lys
     385             390             395             400

15   Thr Thr Tyr Phe Glu Ile Phe Thr Ala Gly Ala Gly Thr Gly Glu Val
                     405             410             415

     Glu Val Val Ile Gln Asp Pro Met Gly Gln Lys Gly Thr Val Glu Pro
                 420             425             430

     Gln Leu Glu Ala Arg Gly Asp Ser Thr Tyr Arg Cys Ser Tyr Gln Pro
20               435             440             445

     Thr Met Glu Gly Val His Thr Val His Val Thr Phe Ala Gly Val Pro
                 450             455             460

     Ile Pro Arg Ser Pro Tyr Thr Val Thr Val Gly Gln Ala Cys Asn Pro
     465             470             475             480
```

```
      Ser Ala Cys Arg Ala Val Gly Arg Gly Leu Gln Pro Lys Gly Val Arg
                      485             490             495

      Val Lys Glu Thr Ala Asp Phe Lys Val Tyr Thr Lys Gly Ala Gly Ser
                      500             505             510

  5   Gly Glu Leu Lys Val Thr Val Lys Gly Pro Lys Gly Glu Glu Arg Val
                      515             520             525

      Lys Gln Lys Asp Leu Gly Asp Gly Val Tyr Gly Phe Glu Tyr Tyr Pro
                      530             535             540

      Met Val Pro Gly Thr Tyr Ile Val Thr Ile Thr Trp Gly Gly Gln Asn
 10   545             550             555             560

      Ile Gly Arg Ser Pro Phe Glu Val Lys Val Gly Thr Glu Cys Gly Asn
                      565             570             575

      Gln Lys Val Arg Ala Trp Gly Pro Gly Leu Glu Gly Gly Val Val Gly
                      580             585             590

 15   Lys Ser Ala Asp Phe Val Val Glu Ala Ile Gly Asp Asp Val Gly Thr
                      595             600             605

      Leu Gly Phe Ser Val Glu Gly Pro Ser Gln Ala Lys Ile Glu Cys Asp
                      610             615             620

      Asp Lys Gly Asp Gly Ser Cys Asp Val Arg Tyr Trp Pro Gln Glu Ala
 20   625             630             635             640

      Gly Glu Tyr Ala Val His Val Leu Cys Asn Ser Glu Asp Ile Arg Leu
                      645             650             655

      Ser Pro Phe Met Ala Asp Ile Arg Asp Ala Pro Gln Asp Phe His Pro
                      660             665             670
```

```
        Asp Arg Val Lys Ala Arg Gly Pro Gly Leu Glu Lys Thr Gly Val Ala
                675                 680                 685

        Val Asn Lys Pro Ala Glu Phe Thr Val Asp Ala Lys His Gly Gly Lys
                690                 695                 700

   5    Ala Pro Leu Arg Val Gln Val Gln Asp Asn Glu Gly Cys Pro Val Glu
        705                 710                 715                 720

        Ala Leu Val Lys Asp Asn Gly Asn Gly Thr Tyr Ser Cys Ser Tyr Val
                        725                 730                 735

        Pro Arg Lys Pro Val Lys His Thr Ala Met Val Ser Trp Gly Gly Val
  10                740                 745                 750

        Ser Ile Pro Asn Ser Pro Phe Arg Val Asn Val Gly Ala Gly Ser His
                755                 760                 765

        Pro Asn Lys Val Lys Val Tyr Gly Pro Gly Val Ala Lys Thr Gly Leu
                770                 775                 780

  15    Lys Ala His Glu Pro Thr Tyr Phe Thr Val Asp Cys Ala Glu Ala Gly
        785                 790                 795                 800

        Gln Gly Asp Val Ser Ile Gly Ile Lys Cys Ala Pro Gly Val Val Gly
                        805                 810                 815

        Pro Ala Glu Ala Asp Ile Asp Phe Asp Ile Ile Arg Asn Asp Asn Asp
  20                820                 825                 830

        Thr Phe Thr Val Lys Tyr Thr Pro Arg Gly Ala Gly Ser Tyr Thr Ile
                835                 840                 845

        Met Val Leu Phe Ala Asp Gln Ala Thr Pro Thr Ser Pro Ile Arg Val
                850                 855                 860
```

Lys Val Glu Pro Ser His Asp Ala Ser Lys Val Lys Ala Glu Gly Pro

865   870   875   880

Gly Leu Ser Arg Thr Gly Val Glu Leu Gly Lys Pro Thr His Phe Thr

885   890   895

5 Val Asn Ala Lys Ala Ala Gly Lys Gly Lys Leu Asp Val Gln Phe Ser

900   905   910

Gly Leu Thr Lys Gly Asp Ala Val Arg Asp Val Asp Ile Ile Asp His

915   920   925

His Asp Asn Thr Tyr Thr Val Lys Tyr Thr Pro Val Gln Gln Gly Pro

10   930   935   940

Val Gly Val Asn Val Thr Tyr Gly Gly Asp Pro Ile Pro Lys Ser Pro

945   950   955   960

Phe Ser Val Ala Val Ser Pro Ser Leu Asp Leu Ser Lys Ile Lys Val

965   970   975

15 Ser Gly Leu Gly Glu Lys Val Asp Val Gly Lys Asp Gln Glu Phe Thr

980   985   990

Val Lys Ser Lys Gly Ala Gly Gly Gln Gly Lys Val Ala Ser Lys Ile

995   1000   1005

Val Gly Pro Ser Gly Ala Ala Val Pro Cys Lys Val Glu Pro Gly

20   1010   1015   1020

Leu Gly Ala Asp Asn Ser Val Val Arg Phe Leu Pro Arg Glu Glu

1025   1030   1035

Gly Pro Tyr Glu Val Glu Val Thr Tyr Asp Gly Val Pro Val Pro

1040   1045   1050

```
    Gly Ser  Pro Phe Pro Leu Glu  Ala Val Ala Pro Thr  Lys Pro Ser
         1055              1060             1065

    Lys Val  Lys Ala Phe Gly Pro  Gly Leu Gln Gly Gly  Ser Ala Gly
         1070              1075             1080

5   Ser Pro  Ala Arg Phe Thr Ile  Asp Thr Lys Gly Ala  Gly Thr Gly
         1085              1090             1095

    Gly Leu  Gly Leu Thr Val Glu  Gly Pro Cys Glu Ala  Gln Leu Glu
         1100              1105             1110

    Cys Leu  Asp Asn Gly Asp Gly  Thr Cys Ser Val Ser  Tyr Val Pro
10       1115              1120             1125

    Thr Glu  Pro Gly Asp Tyr Asn  Ile Asn Ile Leu Phe  Ala Asp Thr
         1130              1135             1140

    His Ile  Pro Gly Ser Pro Phe  Lys Ala His Val Val  Pro Cys Phe
         1145              1150             1155

15  Asp Ala  Ser Lys Val Lys Cys  Ser Gly Pro Gly Leu  Glu Arg Ala
         1160              1165             1170

    Thr Ala  Gly Glu Val Gly Gln  Phe Gln Val Asp Cys  Ser Ser Ala
         1175              1180             1185

    Gly Ser  Ala Glu Leu Thr Ile  Glu Ile Cys Ser Glu  Ala Gly Leu
20       1190              1195             1200

    Pro Ala  Glu Val Tyr Ile Gln  Asp His Gly Asp Gly  Thr His Thr
         1205              1210             1215

    Ile Thr  Tyr Ile Pro Leu Cys  Pro Gly Ala Tyr Thr  Val Thr Ile
         1220              1225             1230
```

```
       Lys Tyr  Gly Gly Gln Pro  Val Pro Asn Phe  Pro Ser  Lys Leu Gln
           1235             1240              1245

       Val Glu  Pro Ala Val Asp  Thr Ser Gly Val  Gln Cys  Tyr Gly Pro
           1250             1255              1260

  5    Gly Ile .Glu Gly Gln Gly  Val Phe Arg Glu  Ala Thr  Thr Glu Phe
           1265             1270              1275

       Ser Val  Asp Ala Arg Ala  Leu Thr Gln Thr  Gly Gly  Pro His Val
           1280             1285              1290

       Lys Ala  Arg Val Ala Asn  Pro Ser Gly Asn  Leu Thr  Glu Thr Tyr
 10        1295             1300              1305

       Val Gln  Asp Arg Gly Asp  Gly Met Tyr Lys  Val Glu  Tyr Thr Pro
           1310             1315              1320

       Tyr Glu  Glu Gly Leu His  Ser Val Asp Val  Thr Tyr  Asp Gly Ser
           1325             1330              1335

 15    Pro Val  Pro Ser Ser Pro  Phe Gln Val Pro  Val Thr  Glu Gly Cys
           1340             1345              1350

       Asp Pro  Ser Arg Val Arg  Val His Gly Pro  Gly Ile  Gln Ser Gly
           1355             1360              1365

       Thr Thr  Asn Lys Pro Asn  Lys Phe Thr Val  Glu Thr  Arg Gly Ala
 20        1370             1375              1380

       Gly Thr  Gly Gly Leu Gly  Leu Ala Val Glu  Gly Pro  Ser Glu Ala
           1385             1390              1395

       Lys Met  Ser Cys Met Asp  Asn Lys Asp Gly  Ser Cys  Ser Val Glu
           1400             1405              1410
```

```
       Tyr Ile  Pro Tyr Glu Ala Gly  Thr Tyr Ser Leu Asn  Val Thr Tyr

            1415              1420              1425

       Gly Gly  His Gln Val Pro Gly  Ser Pro Phe Lys Val  Pro Val His

            1430              1435              1440

    5  Asp Val  Thr Asp Ala Ser Lys  Val Lys Cys Ser Gly  Pro Gly Leu

            1445              1450              1455

       Ser Pro  Gly Met Val Arg Ala  Asn Leu Pro Gln Ser  Phe Gln Val

            1460              1465              1470

       Asp Thr  Ser Lys Ala Gly Val  Ala Pro Leu Gln Val  Lys Val Gln

   10       1475              1480              1485

       Gly Pro  Lys Gly Leu Val Glu  Pro Val Asp Val Val  Asp Asn Ala

            1490              1495              1500

       Asp Gly  Thr Gln Thr Val Asn  Tyr Val Pro Ser Arg  Glu Gly Pro

            1505              1510              1515

   15  Tyr Ser  Ile Ser Val Leu Tyr  Gly Asp Glu Glu Val  Pro Arg Ser

            1520              1525              1530

       Pro Phe  Lys Val Lys Val Leu  Pro Thr His Asp Ala  Ser Lys Val

            1535              1540              1545

       Lys Ala  Ser Gly Pro Gly Leu  Asn Thr Thr Gly Val  Pro Ala Ser

   20       1550              1555              1560

       Leu Pro  Val Glu Phe Thr Ile  Asp Ala Lys Asp Ala  Gly Glu Gly

            1565              1570              1575

       Leu Leu  Ala Val Gln Ile Thr  Asp Pro Glu Gly Lys  Pro Lys Lys

            1580              1585              1590
```

```
         Thr His   Ile Gln Asp Asn His   Asp Gly Thr Tyr   Thr Val Ala Tyr

             1595            1600            1605

   5     Val Pro   Asp Val Thr Gly Arg   Tyr Thr Ile Leu   Ile Lys Tyr Gly

             1610            1615            1620

         Gly Asp   Glu Ile Pro Phe Ser   Pro Tyr Arg Val   Arg Ala Val Pro

             1625            1630            1635

         Thr Gly   Asp Ala Ser Lys Cys   Thr Val Thr Val   Ser Ile Gly Gly

   10        1640            1645            1650

         His Gly   Leu Gly Ala Gly Ile   Gly Pro Thr Ile   Gln Ile Gly Glu

             1655            1660            1665

         Glu Thr   Val Ile Thr Val Asp   Thr Lys Ala Ala   Gly Lys Gly Lys

             1670            1675            1680

   15    Val Thr   Cys Thr Val Cys Thr   Pro Asp Gly Ser   Glu Val Asp Val

             1685            1690            1695

         Asp Val   Val Glu Asn Glu Asp   Gly Thr Phe Asp   Ile Phe Tyr Thr

             1700            1705            1710

         Ala Pro   Gln Pro Gly Lys Tyr   Val Ile Cys Val   Arg Phe Gly Gly

   20        1715            1720            1725

         Glu His   Val Pro Asn Ser Pro   Phe Gln Val Thr   Ala Leu Ala Gly

             1730            1735            1740

         Asp Gln   Pro Ser Val Gln Pro   Pro Leu Arg Ser   Gln Gln Leu Ala

             1745            1750            1755
```

```
        Pro Gln  Tyr Thr Tyr Ala Gln  Gly Gly Gln Gln Thr  Trp Ala Pro

            1760              1765              1770

        Glu Arg  Pro Leu Val Gly Val  Asn Gly Leu Asp Val  Thr Ser Leu

            1775              1780              1785

     5  Arg Pro  Phe Asp Leu Val Ile  Pro Phe Thr Ile Lys  Lys Gly Glu

            1790              1795              1800

        Ile Thr  Gly Glu Val Arg Met  Pro Ser Gly Lys Val  Ala Gln Pro

            1805              1810              1815

        Thr Ile  Thr Asp Asn Lys Asp  Gly Thr Val Thr Val  Arg Tyr Ala

    10      1820              1825              1830

        Pro Ser  Glu Ala Gly Leu His  Glu Met Asp Ile Arg  Tyr Asp Asn

            1835              1840              1845

        Met His  Ile Pro Gly Ser Pro  Leu Gln Phe Tyr Val  Asp Tyr Val

            1850              1855              1860

    15  Asn Cys  Gly His Val Thr Ala  Tyr Gly Pro Gly Leu  Thr His Gly

            1865              1870              1875

        Val Val  Asn Lys Pro Ala Thr  Phe Thr Val Asn Thr  Lys Asp Ala

            1880              1885              1890

        Gly Glu  Gly Gly Leu Ser Leu  Ala Ile Glu Gly Pro  Ser Lys Ala

    20      1895              1900              1905

        Glu Ile  Ser Cys Thr Asp Asn  Gln Asp Gly Thr Cys  Ser Val Ser

            1910              1915              1920

        Tyr Leu  Pro Val Leu Pro Gly  Asp Tyr Ser Ile Leu  Val Lys Tyr

            1925              1930              1935
```

```
     Asn Glu  Gln His Val Pro Gly  Ser Pro Phe Thr Ala  Arg Val Thr

         1940                1945                1950

     Gly Asp  Asp Ser Met Arg Met  Ser His Leu Lys Val  Gly Ser Ala

         1955                1960                1965

  5  Ala Asp  Ile Pro Ile Asn Ile  Ser Glu Thr Asp Leu  Ser Leu Leu

         1970                1975                1980

     Thr Ala  Thr Val Val Pro Pro  Ser Gly Arg Glu Glu  Pro Cys Leu

         1985                1990                1995

     Leu Lys  Arg Leu Arg Asn Gly  His Val Gly Ile Ser  Phe Val Pro

  10     2000                2005                2010

     Lys Glu  Thr Gly Glu His Leu  Val His Val Lys Lys  Asn Gly Gln

         2015                2020                2025

     His Val  Ala Ser Ser Pro Ile  Pro Val Val Ile Ser  Gln Ser Glu

         2030                2035                2040

  15 Ile Gly  Asp Ala Ser Arg Val  Arg Val Ser Gly Gln  Gly Leu His

         2045                2050                2055

     Glu Gly  His Thr Phe Glu Pro  Ala Glu Phe Ile Ile  Asp Thr Arg

         2060                2065                2070

     Asp Ala  Gly Tyr Gly Gly Leu  Ser Leu Ser Ile Glu  Gly Pro Ser

  20     2075                2080                2085

     Lys Val  Asp Ile Asn Thr Glu  Asp Leu Glu Asp Gly  Thr Cys Arg

         2090                2095                2100

     Val Thr  Tyr Cys Pro Thr Glu  Pro Gly Asn Tyr Ile  Ile Asn Ile

         2105                2110                2115
```

```
      Lys Phe  Ala Asp Gln His Val  Pro Gly Ser Pro Phe  Ser Val Lys
           2120              2125              2130

      Val Thr  Gly Glu Gly Arg Val  Lys Glu Ser Ile Thr  Arg Arg Arg
           2135              2140              2145

   5  Arg Ala  Pro Ser Val Ala Asn  Val Gly Ser His Cys  Asp Leu Ser
           2150              2155              2160

      Leu Lys  Ile Pro Glu Ile Ser  Ile Gln Asp Met Thr  Ala Gln Val
           2165              2170              2175

      Thr Ser  Pro Ser Gly Lys Thr  His Glu Ala Glu Ile  Val Glu Gly
  10       2180              2185              2190

      Glu Asn  His Thr Tyr Cys Ile  Arg Phe Val Pro Ala  Glu Met Gly
           2195              2200              2205

      Thr His  Thr Val Ser Val Lys  Tyr Lys Gly Gln His  Val Pro Gly
           2210              2215              2220

  15  Ser Pro  Phe Gln Phe Thr Val  Gly Pro Leu Gly Glu  Gly Gly Ala
           2225              2230              2235

      His Lys  Val Arg Ala Gly Gly  Pro Gly Leu Glu Arg  Ala Glu Ala
           2240              2245              2250

      Gly Val  Pro Ala Glu Phe Ser  Ile Trp Thr Arg Glu  Ala Gly Ala
  20       2255              2260              2265

      Gly Gly  Leu Ala Ile Ala Val  Glu Gly Pro Ser Lys  Ala Glu Ile
           2270              2275              2280

      Ser Phe  Glu Asp Arg Lys Asp  Gly Ser Cys Gly Val  Ala Tyr Val
           2285              2290              2295
```

```
    Val Gln  Glu Pro Gly Asp Tyr  Glu Val Ser Val Lys  Phe Asn Glu
        2300            2305            2310

    Glu His  Ile Pro Asp Ser Pro  Phe Val Val Pro Val  Ala Ser Pro
        2315            2320            2325

5   Ser Gly  Asp Ala Arg Arg Leu  Thr Val Ser Ser Leu  Gln Glu Ser
        2330            2335            2340

    Gly Leu  Lys Val Asn Gln Pro  Ala Ser Phe Ala Val  Ser Leu Asn
        2345            2350            2355

    Gly Ala  Lys Gly Ala Ile Asp  Ala Lys Val His Ser  Pro Ser Gly
10      2360            2365            2370

    Ala Leu  Glu Glu Cys Tyr Val  Thr Glu Ile Asp Gln  Asp Lys Tyr
        2375            2380            2385

    Ala Val  Arg Phe Ile Pro Arg  Glu Asn Gly Val Tyr  Leu Ile Asp
        2390            2395            2400

15  Val Lys  Phe Asn Gly Thr His  Ile Pro Gly Ser Pro  Phe Lys Ile
        2405            2410            2415

    Arg Val  Gly Glu Pro Gly His  Gly Gly Asp Pro Gly  Leu Val Ser
        2420            2425            2430

    Ala Tyr  Gly Ala Gly Leu Glu  Gly Gly Val Thr Gly  Asn Pro Ala
20      2435            2440            2445

    Glu Phe  Val Val Asn Thr Ser  Asn Ala Gly Ala Gly  Ala Leu Ser
        2450            2455            2460

    Val Thr  Ile Asp Gly Pro Ser  Lys Val Lys Met Asp  Cys Gln Glu
        2465            2470            2475
```

```
    Cys Pro  Glu Gly Tyr Arg Val  Thr Tyr Thr Pro Met  Ala Pro Gly

         2480                2485                2490

    Ser Tyr  Leu Ile Ser Ile Lys  Tyr Gly Gly Pro Tyr  His Ile Gly

         2495                2500                2505

5   Gly Ser  Pro Phe Lys Ala Lys  Val Thr Gly Pro Arg  Leu Val Ser

         2510                2515                2520

    Asn His  Ser Leu His Glu Thr  Ser Ser Val Phe Val  Asp Ser Leu

         2525                2530                2535

    Thr Lys  Ala Thr Cys Ala Pro  Gln His Gly Ala Pro  Gly Pro Gly

10       2540                2545                2550

    Pro Ala  Asp Ala Ser Lys Val  Val Ala Lys Gly Leu  Gly Leu Ser

         2555                2560                2565

    Lys Ala  Tyr Val Gly Gln Lys  Ser Ser Phe Thr Val  Asp Cys Ser

         2570                2575                2580

15  Lys Ala  Gly Asn Asn Met Leu  Leu Val Gly Val His  Gly Pro Arg

         2585                2590                2595

    Thr Pro  Cys Glu Glu Ile Leu  Val Lys His Val Gly  Ser Arg Leu

         2600                2605                2610

    Tyr Ser  Val Ser Tyr Leu Leu  Lys Asp Lys Gly Glu  Tyr Thr Leu

20       2615                2620                2625

    Val Val  Lys Trp Gly His Glu  His Ile Pro Gly Ser  Pro Tyr Arg

         2630                2635                2640

    Val Val  Val Pro

         2645
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<210> 10

<211> 199

5   <212> PRT

<213> Homo sapiens

<220>

<221> Transgelin 2

<222> (1)..(199)

10   <223> Accession No. as of 06 Dec 2002: P37802

<400> 10

Met Ala Asn Arg Gly Pro Ala Tyr Gly Leu Ser Arg Glu Val Gln Gln

1   5   10   15

15   Lys Ile Glu Lys Gln Tyr Asp Ala Asp Leu Glu Gln Ile Leu Ile Gln

                20   25   30

Trp Ile Thr Thr Gln Cys Arg Lys Asp Val Gly Arg Pro Gln Pro Gly

            35   40   45

Arg Glu Asn Phe Gln Asn Trp Leu Lys Asp Gly Thr Val Leu Cys Glu

20   50   55   60

Leu Ile Asn Ala Leu Tyr Pro Glu Gly Gln Ala Pro Val Lys Lys Ile

65   70   75   80

Gln Ala Ser Thr Met Ala Phe Lys Gln Met Glu Gln Ile Ser Gln Phe

                85   90   95

Leu Gln Ala Ala Glu Arg Tyr Gly Ile Asn Thr Thr Asp Ile Phe Gln

        100   105   110

Thr Val Asp Leu Trp Glu Gly Lys Asn Met Ala Cys Val Gln Arg Thr

        115   120   125

5 Leu Met Asn Leu Gly Gly Leu Ala Val Ala Arg Asp Asp Gly Leu Phe

        130   135   140

Ser Gly Asp Pro Asn Trp Phe Pro Lys Lys Ser Lys Glu Asn Pro Arg

145   150   155   160

Asn Phe Ser Asp Asn Gln Leu Gln Glu Gly Lys Asn Val Ile Gly Leu

10   165   170   175

Gln Met Gly Thr Asn Arg Gly Ala Ser Gln Ala Gly Met Thr Gly Tyr

        180   185   190

Gly Met Pro Arg Gln Ile Leu

        195

15

<210> 11

<211> 248

<212> PRT

20 <213> Homo sapiens

<220>

<221> Tropomyosin alpha 4 chain

<222> (1)..(248)

<223> Accession No. P07226

<400>   11

Met Ala Gly Leu Asn Ser Leu Glu Ala Val Lys Arg Lys Ile Gln Ala
1   5   10   15

5 Leu Gln Gln Gln Ala Asp Glu Ala Glu Asp Arg Ala Gln Gly Leu Gln
                20   25   30

   Arg Glu Leu Asp Gly Glu Arg Glu Arg Glu Lys Ala Glu Gly Asp
                35   40   45

   Val Ala Ala Leu Asn Arg Arg Ile Gln Leu Val Glu Glu Glu Leu Asp
10   50   55   60

   Arg Ala Gln Glu Arg Leu Ala Thr Ala Leu Gln Lys Leu Glu Glu Ala
   65   70   75   80

   Glu Lys Ala Ala Asp Glu Ser Glu Arg Gly Met Lys Val Ile Glu Asn
                    85   90   95

15 Arg Ala Met Lys Asp Glu Glu Lys Met Glu Ile Gln Glu Met Gln Leu
                    100   105   110

   Lys Glu Ala Lys His Ile Ala Glu Glu Ala Asp Arg Lys Tyr Glu Glu
                    115   120   125

   Val Ala Arg Lys Leu Val Ile Leu Glu Gly Glu Leu Glu Arg Ala Glu
20   130   135   140

   Glu Arg Ala Glu Val Ser Glu Leu Lys Cys Gly Asp Leu Glu Glu Glu
   145   150   155   160

   Leu Lys Asn Val Thr Asn Asn Leu Lys Ser Leu Glu Ala Ala Ser Glu
                    165   170   175

Lys Tyr Ser Glu Lys Glu Asp Lys Tyr Glu Glu Glu Ile Lys Leu Leu

           180   185   190

Ser Asp Lys Leu Lys Glu Ala Glu Thr Arg Ala Glu Phe Ala Glu Arg

           195   200   205

5   Thr Val Ala Lys Leu Glu Lys Thr Ile Asp Asp Leu Glu Glu Lys Leu

           210   215   220

Ala Gln Ala Lys Glu Glu Asn Val Gly Leu His Gln Thr Leu Asp Gln

225   230   235   240

Thr Leu Asn Glu Leu Asn Cys Ile

10   245

<210>   12

<211>   793

15   <212>   PRT

<213>   Homo sapiens

<220>

<221>   Caldesmon

<222>   (1)..(793)

20   <223>   Accession No. as of 06 Dec 2002: Q05682

<400>   12

Met Asp Asp Phe Glu Arg Arg Arg Glu Leu Arg Arg Gln Lys Arg Glu

1   5   10   15

Glu Met Arg Leu Glu Ala Glu Arg Ile Ala Tyr Gln Arg Asn Asp Asp

            20   25   30

Asp Glu Glu Glu Ala Ala Arg Glu Arg Arg Arg Ala Arg Gln Glu

            35   40   45

5   Arg Leu Arg Gln Lys Gln Glu Glu Glu Ser Leu Gly Gln Val Thr Asp

            50   55   60

Gln Val Glu Val Asn Ala Gln Asn Ser Val Pro Asp Glu Glu Ala Lys

    65   70   75   80

Thr Thr Thr Thr Asn Thr Gln Val Glu Gly Asp Asp Glu Ala Ala Phe

10   85   90   95

Leu Glu Arg Leu Ala Arg Arg Glu Glu Arg Arg Gln Lys Arg Leu Gln

            100   105   110

Glu Ala Leu Glu Arg Gln Lys Glu Phe Asp Pro Thr Ile Thr Asp Ala

            115   120   125

15 Ser Leu Ser Leu Pro Ser Arg Arg Met Gln Asn Asp Thr Ala Glu Asn

            130   135   140

Glu Thr Thr Glu Lys Glu Glu Lys Ser Glu Ser Arg Gln Glu Arg Tyr

    145   150   155   160

Glu Ile Glu Glu Thr Glu Thr Val Thr Lys Ser Tyr Gln Lys Asn Asp

20   165   170   175

Trp Arg Asp Ala Glu Glu Asn Lys Lys Glu Asp Lys Glu Lys Glu Glu

            180   185   190

Glu Glu Glu Glu Lys Pro Lys Arg Gly Ser Ile Gly Glu Asn Gln Val

            195   200   205

Glu Val Met Val Glu Glu Lys Thr Thr Glu Ser Gln Glu Glu Thr Val
        210   215   220

Val Met Ser Leu Lys Asn Gly Gln Ile Ser Ser Glu Glu Pro Lys Gln
    225   230   235   240

5   Glu Glu Glu Arg Glu Gln Gly Ser Asp Glu Ile Ser His His Glu Lys
                    245   250   255

Met Glu Glu Glu Asp Lys Glu Arg Ala Glu Ala Glu Arg Ala Arg Leu
                260   265   270

Glu Ala Glu Glu Arg Glu Arg Ile Lys Ala Glu Gln Asp Lys Lys Ile
10   275   280   285

Ala Asp Glu Arg Ala Arg Ile Glu Ala Glu Glu Lys Ala Ala Ala Gln
        290   295   300

Glu Arg Glu Arg Arg Glu Ala Glu Glu Arg Glu Arg Met Arg Glu Glu
    305   310   315   320

15 Glu Lys Arg Ala Ala Glu Glu Arg Gln Arg Ile Lys Glu Glu Glu Lys
                    325   330   335

Arg Ala Ala Glu Glu Arg Gln Arg Ile Lys Glu Glu Glu Lys Arg Ala
        340   345   350

Ala Glu Glu Arg Gln Arg Ile Lys Glu Glu Glu Lys Arg Ala Ala Glu
20   355   360   365

Glu Arg Gln Arg Ala Arg Ala Glu Glu Glu Glu Lys Ala Lys Val Glu
        370   375   380

Glu Gln Lys Arg Asn Lys Gln Leu Glu Glu Lys Lys Arg Ala Met Gln
    385   390   395   400

Glu Thr Lys Ile Lys Gly Glu Lys Val Glu Gln Lys Ile Glu Gly Lys
              405   410   415

    Trp Val Asn Glu Lys Lys Ala Gln Glu Asp Lys Leu Gln Thr Ala Val
                  420   425   430

5 Leu Lys Lys Gln Gly Glu Glu Lys Gly Thr Lys Val Gln Ala Lys Arg
                  435   440   445

    Glu Lys Leu Gln Glu Asp Lys Pro Thr Phe Lys Lys Glu Glu Ile Lys
              450   455   460

    Asp Glu Lys Ile Lys Lys Asp Lys Glu Pro Lys Glu Glu Val Lys Ser
10 465   470   475   480

    Phe Met Asp Arg Lys Lys Gly Phe Thr Glu Val Lys Ser Gln Asn Gly
                  485   490   495

    Glu Phe Met Thr His Lys Leu Lys His Thr Glu Asn Thr Phe Ser Arg
                  500   505   510

15 Pro Gly Gly Arg Ala Ser Val Asp Thr Lys Glu Ala Glu Gly Ala Pro
                  515   520   525

    Gln Val Glu Ala Gly Lys Arg Leu Glu Glu Leu Arg Arg Arg Gly
              530   535   540

    Glu Thr Glu Ser Glu Glu Phe Glu Lys Leu Lys Gln Lys Gln Gln Glu
20 545   550   555   560

    Ala Ala Leu Glu Leu Glu Glu Leu Lys Lys Lys Arg Glu Glu Arg Arg
                  565   570   575

    Lys Val Leu Glu Glu Glu Glu Gln Arg Arg Lys Gln Glu Glu Ala Asp
              580   585   590

Arg Lys Leu Arg Glu Glu Glu Glu Lys Arg Arg Leu Lys Glu Glu Ile
        595   600   605

Glu Arg Arg Arg Ala Glu Ala Ala Glu Lys Arg Gln Lys Met Pro Glu
        610   615   620

5   Asp Gly Leu Ser Asp Asp Lys Lys Pro Phe Lys Cys Phe Thr Pro Lys
    625   630   635   640

Gly Ser Ser Leu Lys Ile Glu Glu Arg Ala Glu Phe Leu Asn Lys Ser
                645   650   655

Val Gln Lys Ser Ser Gly Val Lys Ser Thr His Gln Ala Ala Ile Val
10   660   665   670

Ser Lys Ile Asp Ser Arg Leu Glu Gln Tyr Thr Ser Ala Ile Glu Gly
        675   680   685

Thr Lys Ser Ala Lys Pro Thr Lys Pro Ala Ala Ser Asp Leu Pro Val
        690   695   700

15 Pro Ala Glu Gly Val Arg Asn Ile Lys Ser Met Trp Glu Lys Gly Asn
    705   710   715   720

Val Phe Ser Ser Pro Thr Ala Ala Gly Thr Pro Asn Lys Glu Thr Ala
                725   730   735

Gly Leu Lys Val Gly Val Ser Ser Arg Ile Asn Glu Trp Leu Thr Lys
20   740   745   750

Thr Pro Asp Gly Asn Lys Ser Pro Ala Pro Lys Pro Ser Asp Leu Arg
        755   760   765

Pro Gly Asp Val Ser Ser Lys Arg Asn Leu Trp Glu Lys Gln Ser Val
        770   775   780

```
Asp Lys Val Thr Ser Pro Thr Lys Val

785                      790
```

```
5    <210>   13

     <211>   458

     <212>   PRT

     <213>   Homo sapiens

     <220>

10   <221>   Alpha enolase

     <222>   (1)..(458)

     <223>   Accession No. as of 06 Dec 2002: Q05524

     <400>   13
```

```
15   Met Ser Ile Leu Lys Ile Ile His Ala Arg Asp Ile Phe Glu Ser Arg

     1               5                   10                  15

     Gly Asn Pro Thr Val Glu Val Asp Leu Tyr Thr Asn Lys Gly Gly Leu

                     20                  25                  30

     Phe Gly Arg Ala Ala Val Pro Ser Gly Ala Ser Thr Gly Ile Tyr Glu

20           35                  40                  45

     Ala Leu Leu Glu Leu Arg Asp Asn Asp Lys Thr Arg Tyr Met Gly Gly

             50                  55                  60

     Lys Gly Val Ser Lys Ala Val Glu His Ile Ile Asn Lys Thr Ile Ala

     65                  70                  75                  80
```

Pro Ala Leu Ile Ser Lys Asn Val Asn Val Val Glu Gln Asp Lys Ile
                    85   90   95

Asp Asn Leu Met Leu Asp Met Asp Gly Ser Glu Asn Lys Ser Lys Phe
                  100   105   110

5 Gly Ala Asn Ala Ile Leu Gly Val Ser Leu Ala Val Cys Ser Asn Ala
              115   120   125

   Gly Ala Thr Ala Glu Lys Gly Val Pro Leu Tyr Arg His Ile Ala Asp
           130   135   140

   Leu Ala Gly Asn Asn Pro Glu Val Ile Leu Pro Val Pro Ala Phe Asn
10 145   150   155   160

   Val Ile Asn Gly Gly Ser His Ala Gly Asn Lys Leu Ala Met Gln Glu
                  165   170   175

   Phe Met Ile Pro Pro Cys Gly Ala Asp Arg Phe Asn Asp Ala Ile Arg
                  180   185   190

15 Ile Gly Ala Glu Val Tyr His Asn Leu Lys Asn Val Ile Lys Glu Lys
              195   200   205

   Tyr Gly Lys Asp Ala Thr Asn Val Gly Asp Glu Gly Gly Phe Ala Pro
           210   215   220

   Asn Ile Leu Glu Asn Lys Glu Ala Leu Glu Leu Leu Lys Thr Ala Ile
20 225   230   235   240

   Gly Lys Ala Gly Tyr Ser Asp Lys Val Val Ile Gly Met Asp Val Ala
              245   250   255

   Ala Ser Glu Phe Tyr Arg Asp Gly Lys Tyr Asp Leu Asp Phe Asn Ser
              260   265   270

```
   Pro Asp Asp Pro Ser Arg Tyr Ile Ser Pro Asp Gln Leu Ala Asp Leu
               275             280             285

   Tyr Lys Gly Phe Val Leu Gly His Ala Val Lys Asn Tyr Pro Val Gly
               290             295             300

 5 Val Ser Ile Glu Asp Pro Pro Phe Asp Gln Asp Asp Trp Gly Ala Trp
   305             310             315             320

   Lys Lys Leu Phe Thr Gly Ser Leu Val Gly Ile Gln Val Val Gly Asp
                   325             330             335

   Asp Leu Thr Val Thr Lys Pro Glu Ala Arg Ile Ala Lys Ala Val Glu
10             340             345             350

   Glu Val Lys Ala Cys Asn Cys Leu Leu Leu Leu Lys Val Asn Gln Ile
                   355             360             365

   Gly Ser Val Thr Glu Ser Leu Gln Ala Cys Lys Leu Ala Gln Ser Asn
               370             375             380

15 Gly Trp Gly Val Met Pro Val Ser His Arg Leu Ser Gly Glu Thr Glu
   385             390             395             400

   Asp Thr Phe Met Ala Asp Leu Val Val Gly Leu Cys Thr Gly Gln Ile
                   405             410             415

   Lys Thr Gly Pro Thr Cys Arg Ser Glu Arg Leu Ala Lys Tyr Asn Gln
20             420             425             430

   Leu Leu Arg Ile Glu Glu Ala Glu Ala Gly Ser Lys Ala Arg Phe Ala
               435             440             445

   Gly Arg Asn Phe Arg Asn Pro Arg Ile Asn
               450             455
```

<210> 14

<211> 408

5   <212> PRT

<213> Homo sapiens

<220>

<221> Aminoacylase-1

<222> (1)..(408)

10   <223> Accession No. as of 06 Dec 2002: Q03154

<400> 14

Met Thr Ser Lys Gly Pro Glu Glu Glu His Pro Ser Val Thr Leu Phe

1   5   10   15

15   Arg Gln Tyr Leu Arg Ile Arg Thr Val Gln Pro Lys Pro Asp Tyr Gly

                  20   25   30

Ala Ala Val Ala Phe Phe Glu Glu Thr Ala Arg Gln Leu Gly Leu Gly

         35   40   45

Cys Gln Lys Val Glu Val Ala Pro Gly Tyr Val Val Thr Val Leu Thr

20   50   55   60

Trp Pro Gly Thr Asn Pro Thr Leu Ser Ser Ile Leu Leu Asn Ser His

65   70   75   80

Thr Asp Val Val Pro Val Phe Lys Glu His Trp Ser His Asp Pro Phe

         85   90   95

Glu Ala Phe Lys Asp Ser Glu Gly Tyr Ile Tyr Ala Arg Gly Ala Gln
                100   105   110

Asp Met Lys Cys Val Ser Ile Gln Tyr Leu Glu Ala Val Arg Arg Leu
                115   120   125

5 Lys Val Glu Gly His Arg Phe Pro Arg Thr Ile His Met Thr Phe Val
                130   135   140

Pro Asp Glu Glu Val Gly Gly His Gln Gly Met Glu Leu Phe Val Gln
                145   150   155   160

Arg Pro Glu Phe His Ala Leu Arg Ala Gly Phe Ala Leu Asp Glu Gly
10   165   170   175

Ile Ala Asn Pro Thr Asp Ala Phe Thr Val Phe Tyr Ser Glu Arg Ser
                180   185   190

Pro Trp Trp Val Arg Val Thr Ser Thr Gly Arg Pro Gly His Ala Ser
                195   200   205

15 Arg Phe Met Glu Asp Thr Ala Ala Glu Lys Leu His Lys Val Val Asn
                210   215   220

Ser Ile Leu Ala Phe Arg Glu Lys Glu Trp Gln Arg Leu Gln Ser Asn
    225   230   235   240

Pro His Leu Lys Glu Gly Ser Val Thr Ser Val Asn Leu Thr Lys Leu
20   245   250   255

Glu Gly Gly Val Ala Tyr Asn Val Ile Pro Ala Thr Met Ser Ala Ser
                260   265   270

Phe Asp Phe Arg Val Ala Pro Asp Val Asp Phe Lys Ala Phe Glu Glu
                275   280   285

```
    Gln Leu Gln Ser Trp Cys Gln Ala Ala Gly Glu Gly Val Thr Leu Glu

            290              295              300

    Phe Ala Gln Lys Trp Met His Pro Gln Val Thr Pro Thr Asp Asp Ser

    305              310              315              320

5   Asn Pro Trp Trp Ala Ala Phe Ser Arg Val Cys Lys Asp Met Asn Leu

                     325              330              335

    Thr Leu Glu Pro Glu Ile Met Pro Ala Ala Thr Asp Asn Arg Tyr Ile

                     340              345              350

    Arg Ala Val Gly Val Pro Ala Leu Gly Phe Ser Pro Met Asn Arg Thr

10           355              360              365

    Pro Val Leu Leu His Asp His Asp Glu Arg Leu His Glu Ala Val Phe

            370              375              380

    Leu Arg Gly Val Asp Ile Tyr Thr Arg Leu Leu Pro Ala Leu Ala Ser

    385              390              395              400

15  Val Pro Ala Leu Pro Ser Asp Ser

                405
```

```
    <210>  15

20  <211>  277

    <212>  PRT

    <213>  Homo sapiens

    <220>

    <221>  F-actin capping protein beta subunit
```

<222>   (1)..(277)

<223>   Accession No. as of 06 Dec 2002: P47756

<400>   15

5   Met Ser Asp Gln Gln Leu Asp Cys Ala Leu Asp Leu Met Arg Arg Leu

     1   5   10   15

     Pro Pro Gln Gln Ile Glu Lys Asn Leu Ser Asp Leu Ile Asp Leu Val

                     20   25   30

     Pro Ser Leu Cys Glu Asp Leu Leu Ser Ser Val Asp Gln Pro Leu Lys

10   35   40   45

     Ile Ala Arg Asp Lys Val Val Gly Lys Asp Tyr Leu Leu Cys Asp Tyr

             50   55   60

     Asn Arg Asp Gly Asp Ser Tyr Arg Ser Pro Trp Ser Asn Lys Tyr Asp

     65   70   75   80

15   Pro Pro Leu Glu Asp Gly Ala Met Pro Ser Ala Arg Leu Arg Lys Leu

                     85   90   95

     Glu Val Glu Ala Asn Asn Ala Phe Asp Gln Tyr Arg Asp Leu Tyr Phe

                     100   105   110

     Glu Gly Gly Val Ser Ser Val Tyr Leu Trp Asp Leu Asp His Gly Phe

20   115   120   125

     Ala Gly Val Ile Leu Ile Lys Lys Ala Gly Asp Gly Ser Lys Lys Ile

             130   135   140

     Lys Gly Cys Trp Asp Ser Ile His Val Val Glu Val Gln Glu Lys Ser

     145   150   155   160

Ser Gly Arg Thr Ala His Tyr Lys Leu Thr Ser Thr Val Met Leu Trp

        165   170   175

Leu Gln Thr Asn Lys Ser Gly Ser Gly Thr Met Asn Leu Gly Gly Ser

        180   185   190

5 Leu Thr Arg Gln Met Glu Lys Asp Glu Thr Val Ser Asp Cys Ser Pro

        195   200   205

His Ile Ala Asn Ile Gly Arg Leu Val Glu Asp Met Glu Asn Lys Ile

        210   215   220

Arg Ser Thr Leu Asn Glu Ile Tyr Phe Gly Lys Thr Lys Asp Ile Val

10 225   230   235   240

Asn Gly Leu Arg Ser Ile Asp Ala Ile Pro Asp Asn Gln Lys Phe Lys

        245   250   255

Gln Leu Gln Arg Glu Leu Ser Gln Val Leu Thr Gln Arg Gln Ile Tyr

        260   265   270

15 Ile Gln Pro Asp Asn

        275

<210>   16

20 <211>   289

<212>   PRT

<213>   Homo sapiens

<220>

<221>   Inorganic pyrophosphatase

<222> (1)..(289)

<223> Accession No. as of 06 Dec 2002: Q15181

<400> 16

5   Met Ser Gly Phe Ser Thr Glu Glu Arg Ala Ala Pro Phe Ser Leu Glu
    1   5   10   15

    Tyr Arg Val Phe Leu Lys Asn Glu Lys Gly Gln Tyr Ile Ser Pro Phe
                    20   25   30

    His Asp Ile Pro Ile Tyr Ala Asp Lys Asp Val Phe His Met Val Val
10   35   40   45

    Glu Val Pro Arg Trp Ser Asn Ala Lys Met Glu Ile Ala Thr Lys Asp
                50   55   60

    Pro Leu Asn Pro Ile Lys Gln Asp Val Lys Lys Gly Lys Leu Arg Tyr
    65   70   75   80

15 Val Ala Asn Leu Phe Pro Tyr Lys Gly Tyr Ile Trp Asn Tyr Gly Ala
                    85   90   95

    Ile Pro Gln Thr Trp Glu Asp Pro Gly His Asn Asp Lys His Thr Gly
                    100   105   110

    Cys Cys Gly Asp Asn Asp Pro Ile Asp Val Cys Glu Ile Gly Ser Lys
20   115   120   125

    Val Cys Ala Arg Gly Glu Ile Ile Gly Val Lys Val Leu Gly Ile Leu
                130   135   140

    Ala Met Ile Asp Glu Gly Glu Thr Asp Trp Lys Val Ile Ala Ile Asn
    145   150   155   160

```
    Val Asp Asp Pro Asp Ala Ala Asn Tyr Asn Asp Ile Asn Asp Val Lys
                    165                 170                 175

    Arg Leu Lys Pro Gly Tyr Leu Glu Ala Thr Val Asp Trp Phe Arg Arg
                    180                 185                 190

  5 Tyr Lys Val Pro Asp Gly Lys Pro Glu Asn Glu Phe Ala Phe Asn Ala
                    195                 200                 205

    Glu Phe Lys Asp Lys Asp Phe Ala Ile Asp Ile Ile Lys Ser Thr His
                    210                 215                 220

    Asp His Trp Lys Ala Leu Val Thr Lys Lys Thr Asn Gly Lys Gly Ile
 10 225                 230                 235                 240

    Ser Cys Met Asn Thr Thr Leu Ser Glu Ser Pro Phe Lys Cys Asp Pro
                    245                 250                 255

    Asp Ala Ala Arg Ala Ile Val Asp Ala Leu Pro Pro Pro Cys Glu Ser
                    260                 265                 270

 15 Ala Cys Thr Val Pro Thr Asp Val Asp Lys Trp Phe His His Gln Lys
                    275                 280                 285

    Asn
```

20

    <210> 17

    <211> 250

    <212> PRT

    <213> Homo sapiens

<220>

<221>   Galectin-3 (Galactose-specific lectin 3)

<222>   (1)..(250)

<223>   Accession No. as of 06 Dec 2002: P17931

5   <400>   17

Met Ala Asp Asn Phe Ser Leu His Asp Ala Leu Ser Gly Ser Gly Asn

1   5   10   15

Pro Asn Pro Gln Gly Trp Pro Gly Ala Trp Gly Asn Gln Pro Ala Gly

10   20   25   30

Ala Gly Gly Tyr Pro Gly Ala Ser Tyr Pro Gly Ala Tyr Pro Gly Gln

           35   40   45

Ala Pro Pro Gly Ala Tyr Pro Gly Gln Ala Pro Pro Gly Ala Tyr His

           50   55   60

15 Gly Ala Pro Gly Ala Tyr Pro Gly Ala Pro Ala Pro Gly Val Tyr Pro

65   70   75   80

Gly Pro Pro Ser Gly Pro Gly Ala Tyr Pro Ser Ser Gly Gln Pro Ser

           85   90   95

Ala Pro Gly Ala Tyr Pro Ala Thr Gly Pro Tyr Gly Ala Pro Ala Gly

20   100   105   110

Pro Leu Ile Val Pro Tyr Asn Leu Pro Leu Pro Gly Gly Val Val Pro

           115   120   125

Arg Met Leu Ile Thr Ile Leu Gly Thr Val Lys Pro Asn Ala Asn Arg

           130   135   140

```
      Ile Ala Leu Asp Phe Gln Arg Gly Asn Asp Val Ala Phe His Phe Asn

      145               150               155               160

      Pro Arg Phe Asn Glu Asn Asn Arg Arg Val Ile Val Cys Asn Thr Lys

                        165               170               175

   5  Leu Asp Asn Asn Trp Gly Arg Glu Glu Arg Gln Ser Val Phe Pro Phe

                        180               185               190

      Glu Ser Gly Lys Pro Phe Lys Ile Gln Val Leu Val Glu Pro Asp His

                        195               200               205

      Phe Lys Val Ala Val Asn Asp Ala His Leu Leu Gln Tyr Asn His Arg

  10        210               215               220

      Val Lys Lys Leu Asn Glu Ile Ser Lys Leu Gly Ile Ser Gly Asp Ile

      225               230               235               240

      Asp Leu Thr Ser Ala Ser Tyr Thr Met Ile

                        245               250
```

15


```
      <210>  18

      <211>  347

      <212>  PRT

  20  <213>  Homo sapiens

      <220>

      <221>  Voltage-dependent anion-selective channel protein 2 (VDAC-2)

      <222>  (1)..(347)

      <223>  Accession No.as of 06 Dec 2002: P45880
```

<400>   18

Met Ser Trp Cys Asn Glu Leu Arg Leu Pro Ala Leu Lys Gln His Ser
1   5   10   15

5   Ile Gly Arg Gly Leu Glu Ser His Ile Thr Met Cys Ile Pro Pro Ser
                20   25   30

    Tyr Ala Asp Leu Gly Lys Ala Ala Arg Asp Ile Phe Asn Lys Gly Phe
                35   40   45

    Gly Phe Gly Leu Val Lys Leu Asp Val Lys Thr Lys Ser Cys Ser Gly
10   50   55   60

    Val Glu Phe Ser Thr Ser Gly Ser Ser Asn Thr Asp Thr Gly Lys Val
    65   70   75   80

    Thr Gly Thr Leu Glu Thr Lys Tyr Lys Trp Cys Glu Tyr Gly Leu Thr
                85   90   95

15 Phe Thr Glu Lys Trp Asn Thr Asp Asn Thr Leu Gly Thr Glu Ile Ala
                100   105   110

    Ile Glu Asp Gln Ile Cys Gln Gly Leu Lys Leu Thr Phe Asp Thr Thr
                115   120   125

    Phe Ser Pro Asn Thr Gly Lys Lys Ser Gly Lys Ile Lys Ser Ser Tyr
20   130   135   140

    Lys Arg Glu Cys Ile Asn Leu Gly Cys Asp Val Asp Phe Asp Phe Ala
    145   150   155   160

    Gly Pro Ala Ile His Gly Ser Ala Val Phe Gly Tyr Glu Gly Trp Leu
                165   170   175

Ala Gly Tyr Gln Met Thr Phe Asp Ser Ala Lys Ser Lys Leu Thr Arg
              180   185   190

Asn Asn Phe Ala Val Gly Tyr Arg Thr Gly Asp Phe Gln Leu His Thr
              195   200   205

5 Asn Val Asn Asp Gly Thr Glu Phe Gly Gly Ser Ile Tyr Gln Lys Val
              210   215   220

Cys Glu Asp Leu Asp Thr Ser Val Asn Leu Ala Trp Thr Ser Gly Thr
   225   230   235   240

Asn Cys Thr Arg Phe Gly Ile Ala Ala Lys Tyr Gln Leu Asp Pro Thr
10   245   250   255

Ala Ser Ile Ser Ala Lys Val Asn Asn Ser Ser Leu Ile Gly Val Gly
              260   265   270

Tyr Thr Gln Thr Leu Arg Pro Gly Val Lys Leu Thr Leu Ser Ala Leu
              275   280   285

15 Val Asp Gly Lys Ser Ile Asn Ala Gly Gly His Lys Val Gly Ser Pro
              290   295   300

Trp Ser Trp Arg Leu Asn Pro Ala Glu Arg Asn Leu Trp Glu Trp Ile
   305   310   315   320

Ser Glu Asp Leu Ala Leu Ile Tyr Phe His Cys Asp Gln Gln Gln Ala
20   325   330   335

Phe Phe Pro Pro Glu Asp Asp Gln Asn Lys Gly
              340   345

```
      <210>  19

      <211>  339

      <212>  PRT

      <213>  Homo sapiens

 5    <220>

      <221>  Annexin II

      <222>  (1)..(339)

      <223>  Accession No. as of 06 Dec 2002: P07355

      <400>  19

10


      Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Asp

      1               5                   10                  15

      His Ser Thr Pro Pro Ser Ala Tyr Gly Ser Val Lys Ala Tyr Thr Asn

                      20                  25                  30

15    Phe Asp Ala Glu Arg Asp Ala Leu Asn Ile Glu Thr Ala Ile Lys Thr

                  35                  40                  45

      Lys Gly Val Asp Glu Val Thr Ile Val Asn Ile Leu Thr Asn Arg Ser

              50                  55                  60

      Asn Ala Gln Arg Gln Asp Ile Ala Phe Ala Tyr Gln Arg Arg Thr Lys

20    65                  70                  75                  80

      Lys Glu Leu Ala Ser Ala Leu Lys Ser Ala Leu Ser Gly His Leu Glu

                      85                  90                  95

      Thr Val Ile Leu Gly Leu Leu Lys Thr Pro Ala Gln Tyr Asp Ala Ser

                      100                 105                 110
```

Glu Leu Lys Ala Ser Met Lys Gly Leu Gly Thr Asp Glu Asp Ser Leu
        115   120   125

Ile Glu Ile Ile Cys Ser Arg Thr Asn Gln Glu Leu Gln Glu Ile Asn
        130   135   140

5   Arg Val Tyr Lys Glu Met Tyr Lys Thr Asp Leu Glu Lys Asp Ile Ile
        145   150   155   160

Ser Asp Thr Ser Gly Asp Phe Arg Lys Leu Met Val Ala Leu Ala Lys
                    165   170   175

Gly Arg Arg Ala Glu Asp Gly Ser Val Ile Asp Tyr Glu Leu Ile Asp
10   180   185   190

Gln Asp Ala Arg Asp Leu Tyr Asp Ala Gly Val Lys Arg Lys Gly Thr
                    195   200   205

Asp Val Pro Lys Trp Ile Ser Ile Met Thr Glu Arg Ser Val Pro His
        210   215   220

15   Leu Gln Lys Val Phe Asp Arg Tyr Lys Ser Tyr Ser Pro Tyr Asp Met
        225   230   235   240

Leu Glu Ser Ile Arg Lys Glu Val Lys Gly Asp Leu Glu Asn Ala Phe
                    245   250   255

Leu Asn Leu Val Gln Cys Ile Gln Asn Lys Pro Leu Tyr Phe Ala Asp
20   260   265   270

Arg Leu Tyr Asp Ser Met Lys Gly Lys Gly Thr Arg Asp Lys Val Leu
                    275   280   285

Ile Arg Ile Met Val Ser Arg Ser Glu Val Asp Met Leu Lys Ile Arg
        290   295   300

Ser Glu Phe Lys Arg Lys Tyr Gly Lys Ser Leu Tyr Tyr Tyr Ile Gln

305   310   315   320

Gln Asp Thr Lys Gly Asp Tyr Gln Lys Ala Leu Leu Tyr Leu Cys Gly

                325   330   335

5   Gly Asp Asp

        <210>   20

10   <211>   418

        <212>   PRT

        <213>   Homo sapiens

        <220>

        <221>   Collagen-binding protein 2 precursor

15   <222>   (1)..(418)

        <223>   Accession No. as of 06 Dec 2002: P50454

        <400>   20

    Met Arg Ser Leu Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala

20 1   5   10   15

    Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Pro Gly Thr

                20   25   30

    Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Ser Ala

                35   40   45

Gly Leu Ala Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val
        50   55   60

Glu Asn Ile Leu Val Ser Pro Val Val Val Ala Ser Ser Leu Gly Leu
        65   70   75   80

5   Val Ser Leu Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val
                    85   90   95

Leu Ser Ala Glu Gln Leu Arg Asp Glu Glu Val His Ala Gly Leu Gly
            100   105   110

Glu Leu Leu Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp
10   115   120   125

Lys Leu Gly Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp
            130   135   140

Asp Phe Val Arg Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys
    145   150   155   160

15 Ile Asn Phe Arg Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp
                    165   170   175

Ala Ala Gln Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val
            180   185   190

Glu Arg Thr Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro
20   195   200   205

His Trp Asp Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe
        210   215   220

Met Val Thr Arg Ser Tyr Thr Val Gly Val Met Met Met His Arg Thr
    225   230   235   240

Gly Leu Tyr Asn Tyr Tyr Asp Asp Glu Lys Glu Lys Leu Gln Ile Val

                    245   250   255

Glu Met Pro Leu Ala His Lys Leu Ser Ser Leu Ile Ile Leu Met Pro

                    260   265   270

 5 His His Val Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu

                    275   280   285

Gln Leu Lys Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile

                    290   295   300

Ser Leu Pro Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His

10 305   310   315   320

Leu Ala Gly Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp

                    325   330   335

Leu Ser Arg Met Ser Gly Lys Lys Asp Leu Tyr Leu Ala Ser Val Phe

                    340   345   350

15 His Ala Thr Ala Phe Glu Leu Asp Thr Asp Gly Asn Pro Phe Asp Gln

                    355   360   365

Asp Ile Tyr Gly Arg Glu Glu Leu Arg Ser Pro Lys Leu Phe Tyr Ala

                    370   375   380

Asp His Pro Phe Ile Phe Leu Val Arg Asp Thr Gln Ser Gly Ser Leu

20 385   390   395   400

Leu Phe Ile Gly Arg Leu Val Arg Pro Lys Gly Asp Lys Met Arg Asp

                    405   410   415

Glu Leu

<210> 21

<211> 166

5   <212> PRT

<213> Homo sapiens

<220>

<221> Cofilin, non-muscle isoform

<222> (1)..(166)

10 <223> Accession No. as of 08 ec 2002: P23528

<400> 21

Met Ala Ser Gly Val Ala Val Ser Asp Gly Val Ile Lys Val Phe Asn

1   5   10   15

15 Asp Met Lys Val Arg Lys Ser Ser Thr Pro Glu Glu Val Lys Lys Arg

                20   25   30

Lys Lys Ala Val Leu Phe Cys Leu Ser Glu Asp Lys Lys Asn Ile Ile

        35   40   45

Leu Glu Glu Gly Lys Glu Ile Leu Val Gly Asp Val Gly Gln Thr Val

20   50   55   60

Asp Asp Pro Tyr Ala Thr Phe Val Lys Met Leu Pro Asp Lys Asp Cys

65   70   75   80

Arg Tyr Ala Leu Tyr Asp Ala Thr Tyr Glu Thr Lys Glu Ser Lys Lys

                85   90   95

Glu Asp Leu Val Phe Ile Phe Trp Ala Pro Glu Ser Ala Pro Leu Lys

                100   105   110

Ser Lys Met Ile Tyr Ala Ser Ser Lys Asp Ala Ile Lys Lys Lys Leu

                115   120   125

5 Thr Gly Ile Lys His Glu Leu Gln Ala Asn Cys Tyr Glu Glu Val Lys

                130   135   140

Asp Arg Cys Thr Leu Ala Glu Lys Leu Gly Gly Ser Ala Val Ile Ser

145   150   155   160

Leu Glu Gly Lys Pro Leu

10   165

<210> 22

<211> 165

15 <212> PRT

<213> Homo sapiens

<220>

<221> Peptidyl-prolyl cis-trans isomerase A

<222> (1)..(165)

20 <223> Accession No. as of 09 Dec 2002: P05092

<400> 22

Met Val Asn Pro Thr Val Phe Phe Asp Ile Ala Val Asp Gly Glu Pro

1   5   10   15

```
    Leu Gly Arg Val Ser Phe Glu Leu Phe Ala Asp Lys Val Pro Lys Thr
              20                  25                  30

    Ala Glu Asn Phe Arg Ala Leu Ser Thr Gly Glu Lys Gly Phe Gly Tyr
              35                  40                  45

 5  Lys Gly Ser Cys Phe His Arg Ile Ile Pro Gly Phe Met Cys Gln Gly
              50                  55                  60

    Gly Asp Phe Thr Arg His Asn Gly Thr Gly Gly Lys Ser Ile Tyr Gly
    65                  70                  75                  80

    Glu Lys Phe Glu Asp Glu Asn Phe Ile Leu Lys His Thr Gly Pro Gly
 10                 85                  90                  95

    Ile Leu Ser Met Ala Asn Ala Gly Pro Asn Thr Asn Gly Ser Gln Phe
                     100                 105                 110

    Phe Ile Cys Thr Ala Lys Thr Glu Trp Leu Asp Gly Lys His Val Val
                     115                 120                 125

 15 Phe Gly Lys Val Lys Glu Gly Met Asn Ile Val Glu Ala Met Glu Arg
                     130                 135                 140

    Phe Gly Ser Arg Asn Gly Lys Thr Ser Lys Lys Ile Thr Ile Ala Asp
    145                 150                 155                 160

    Cys Gly Gln Leu Glu
 20                 165
```

```
<210>  23

<211>  638
```

<212>   PRT

<213>   Homo sapiens

<220>

<221>   Dynein intermediate chain 2, cytosolic

5   <222>   (1)..(638)

<223>   Accession No. as of 09 Dec 2002: Q13409

<400>   23

Met Ser Asp Lys Ser Glu Leu Lys Ala Glu Leu Glu Arg Lys Lys Gln

10 1   5   10   15

Arg Leu Ala Gln Ile Arg Glu Glu Lys Lys Arg Lys Glu Glu Glu Arg

                20   25   30

Lys Lys Lys Glu Thr Asp Gln Lys Lys Glu Ala Val Ala Pro Val Gln

                35   40   45

15 Glu Glu Ser Asp Leu Glu Lys Lys Arg Arg Glu Ala Glu Ala Leu Leu

            50   55   60

Gln Ser Met Gly Leu Thr Pro Glu Ser Pro Ile Val Phe Ser Glu Tyr

65   70   75   80

Trp Val Pro Pro Pro Met Ser Pro Ser Ser Lys Ser Val Ser Thr Pro

20   85   90   95

Ser Glu Ala Gly Ser Gln Asp Ser Gly Asp Gly Ala Val Gly Ser Arg

                100   105   110

Thr Leu His Trp Asp Thr Asp Pro Ser Val Leu Gln Leu His Ser Asp

                115   120   125

Ser Asp Leu Gly Arg Gly Pro Ile Lys Leu Gly Met Ala Lys Ile Thr
        130   135   140

Gln Val Asp Phe Pro Pro Arg Glu Ile Val Thr Tyr Thr Lys Glu Thr
    145   150   155   160

5   Gln Thr Pro Val Met Ala Gln Pro Lys Glu Asp Glu Glu Glu Asp Asp
                    165   170   175

Asp Val Val Ala Pro Lys Pro Pro Ile Glu Pro Glu Glu Glu Lys Thr
            180   185   190

Leu Lys Lys Asp Glu Glu Asn Asp Ser Lys Ala Pro Pro His Glu Leu
10   195   200   205

Thr Glu Glu Glu Lys Gln Gln Ile Leu His Ser Glu Glu Phe Leu Ser
        210   215   220

Phe Phe Asp His Ser Thr Arg Ile Val Glu Arg Ala Leu Ser Glu Gln
    225   230   235   240

15 Ile Asn Ile Phe Phe Asp Tyr Ser Gly Arg Asp Leu Glu Asp Lys Glu
                    245   250   255

Gly Glu Ile Gln Ala Gly Ala Lys Leu Ser Leu Asn Arg Gln Phe Phe
            260   265   270

Asp Glu Arg Trp Ser Lys His Arg Val Val Ser Cys Leu Asp Trp Ser
20   275   280   285

Ser Gln Tyr Pro Glu Leu Leu Val Ala Ser Tyr Asn Asn Asn Glu Asp
        290   295   300

Ala Pro His Glu Pro Asp Gly Val Ala Leu Val Trp Asn Met Lys Tyr
    305   310   315   320

```
     Lys Lys Thr Thr Pro Glu Tyr Val Phe His Cys Gln Ser Ala Val Met
                     325             330             335

     Ser Ala Thr Phe Ala Lys Phe His Pro Asn Leu Val Val Gly Gly Thr
                     340             345             350

 5   Tyr Ser Gly Gln Ile Val Leu Trp Asp Asn Arg Ser Asn Lys Arg Thr
                     355             360             365

     Pro Val Gln Arg Thr Pro Leu Ser Ala Ala Ala His Thr His Pro Val
                     370             375             380

     Tyr Cys Val Asn Val Val Gly Thr Gln Asn Ala His Asn Leu Ile Ser
10   385             390             395             400

     Ile Ser Thr Asp Gly Lys Ile Cys Ser Trp Ser Leu Asp Met Leu Ser
                     405             410             415

     His Pro Gln Asp Ser Met Glu Leu Val His Lys Gln Ser Lys Ala Val
                     420             425             430

15   Ala Val Thr Ser Met Ser Phe Pro Val Gly Asp Val Asn Asn Phe Val
                     435             440             445

     Val Gly Ser Glu Glu Gly Ser Val Tyr Thr Ala Cys Arg His Gly Ser
                     450             455             460

     Lys Ala Gly Ile Ser Glu Met Phe Glu Gly His Gln Gly Pro Ile Thr
20   465             470             475             480

     Gly Ile His Cys His Ala Ala Val Gly Ala Val Asp Phe Ser His Leu
                     485             490             495

     Phe Val Thr Ser Ser Phe Asp Trp Thr Val Lys Leu Trp Thr Thr Lys
                     500             505             510
```

```
     Asn Asn Lys Pro Leu Tyr Ser Phe Glu Asp Asn Ala Asp Tyr Val Tyr
             515                 520                 525

     Asp Val Met Trp Ser Pro Thr His Pro Ala Leu Phe Ala Cys Val Asp
             530                 535                 540

  5  Gly Met Gly Arg Leu Asp Leu Trp Asn Leu Asn Asn Asp Thr Glu Val
     545                 550                 555                 560

     Pro Thr Ala Ser Ile Ser Val Glu Gly Asn Pro Ala Leu Asn Arg Val
                         565                 570                 575

     Arg Trp Thr His Ser Gly Arg Glu Ile Ala Val Gly Asp Ser Glu Gly
 10                  580                 585                 590

     Gln Ile Val Ile Tyr Asp Val Gly Glu Gln Ile Ala Val Pro Arg Asn
                 595                 600                 605

     Asp Glu Trp Ala Arg Phe Gly Arg Thr Leu Ala Glu Ile Asn Ala Asn
             610                 615                 620

 15  Arg Ala Asp Ala Glu Glu Glu Ala Ala Thr Arg Ile Pro Ala
     625                 630                 635
```

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     <210>  24

 20  <211>  328

     <212>  PRT

     <213>  Homo sapiens

     <220>

     <221>  Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor
```

<222>   (1)..(328)

<223>   Accession No. as of 09 Dec 2002: Q13011

<400>   24

```
 5  Met Ala Ala Gly Ile Val Ala Ser Arg Arg Leu Arg Asp Leu Leu Thr
     1               5                   10                  15

    Arg Arg Leu Thr Gly Ser Asn Tyr Pro Gly Leu Ser Ile Ser Leu Arg
                    20                  25                  30

    Leu Thr Gly Ser Ser Ala Gln Glu Glu Ala Ser Gly Val Ala Leu Gly
10                  35                  40                  45

    Glu Ala Pro Asp His Ser Tyr Glu Ser Leu Arg Val Thr Ser Ala Gln
                    50                  55                  60

    Lys His Val Leu His Val Gln Leu Asn Arg Pro Asn Lys Arg Asn Ala
                65                  70                  75                  80

15  Met Asn Lys Val Phe Trp Arg Glu Met Val Glu Cys Phe Asn Lys Ile
                        85                  90                  95

    Ser Arg Asp Ala Asp Cys Arg Ala Val Val Ile Ser Gly Ala Gly Lys
                    100                 105                 110

    Met Phe Thr Ala Gly Ile Asp Leu Met Asp Met Ala Ser Asp Ile Leu
20                  115                 120                 125

    Gln Pro Lys Gly Asp Asp Val Ala Arg Ile Ser Trp Tyr Leu Arg Asp
                    130                 135                 140

    Ile Ile Thr Arg Tyr Gln Glu Thr Phe Asn Val Ile Glu Arg Cys Pro
                145                 150                 155                 160
```

Lys Pro Val Ile Ala Ala Val His Gly Gly Cys Ile Gly Gly Gly Val
165   170   175

Asp Leu Val Thr Ala Cys Asp Ile Arg Tyr Cys Ala Gln Asp Ala Phe
180   185   190

5   Phe Gln Val Lys Glu Val Asp Val Gly Leu Ala Ala Asp Val Gly Thr
195   200   205

Leu Glu Arg Leu Pro Lys Val Ile Gly Asn Gln Ser Leu Val Asn Glu
210   215   220

Leu Ala Phe Thr Ala His Lys Met Met Ala Asp Glu Ala Leu Asp Ser
10   225   230   235   240

Gly Leu Val Ser Arg Val Phe Pro Asp Lys Glu Val Met Leu Asp Ala
245   250   255

Ala Leu Pro Leu Ala Pro Glu Ile Ser Ser Lys Thr Thr Val Leu Val
260   265   270

15   Gln Ser Thr Lys Val Asn Leu Leu Tyr Ser Arg Asp His Ser Val Ala
275   280   285

Glu Ser Leu Asn Tyr Val Ala Ser Trp Asn Met Ser Met Leu Gln Thr
290   295   300

Gln Asp Leu Val Lys Ser Val Gln Pro Thr Thr Glu Asn Lys Glu Leu
20   305   310   315   320

Lys Thr Val Thr Phe Ser Lys Leu

325

<210> 25

<211> 1657

<212> PRT

<213> Homo sapiens

5 <220>

<221> Ras GTPase-activating-like protein IQGAP1

<222> (1)..(1657)

<223> Accession No. as of 09 Dec 2002: P46940

<400> 25

10

Met Ser Ala Ala Asp Glu Val Asp Gly Leu Gly Val Ala Arg Pro His
1   5   10   15

Tyr Gly Ser Val Leu Asp Asn Glu Arg Leu Thr Ala Glu Glu Met Asp
                20   25   30

15 Glu Arg Arg Arg Gln Asn Val Ala Tyr Glu Tyr Leu Cys His Leu Glu
                35   40   45

Glu Ala Lys Arg Trp Met Glu Ala Cys Leu Gly Glu Asp Leu Pro Pro
        50   55   60

Thr Thr Glu Leu Glu Glu Gly Leu Arg Asn Gly Val Tyr Leu Ala Lys
20 65   70   75   80

Leu Gly Asn Phe Phe Ser Pro Lys Val Val Ser Leu Lys Lys Ile Tyr
                    85   90   95

Asp Arg Glu Gln Thr Arg Tyr Lys Ala Thr Gly Leu His Phe Arg His
                    100   105   110

Thr Asp Asn Val Ile Gln Trp Leu Asn Ala Met Asp Glu Ile Gly Leu
        115   120   125

Pro Lys Ile Phe Tyr Pro Glu Thr Thr Asp Ile Tyr Asp Arg Lys Asn
        130   135   140

5   Met Pro Arg Cys Ile Tyr Cys Ile His Ala Leu Ser Leu Tyr Leu Phe
        145   150   155   160

Lys Leu Gly Leu Ala Pro Gln Ile Gln Asp Leu Tyr Gly Lys Val Asp
                165   170   175

Phe Thr Glu Glu Glu Ile Asn Asn Met Lys Thr Glu Leu Glu Lys Tyr
10   180   185   190

Gly Ile Gln Met Pro Ala Phe Ser Lys Ile Gly Gly Ile Leu Ala Asn
                195   200   205

Glu Leu Ser Val Asp Glu Ala Ala Leu His Ala Ala Val Ile Ala Ile
        210   215   220

15 Asn Glu Ala Ile Asp Arg Arg Ile Pro Ala Asp Thr Phe Ala Ala Leu
        225   230   235   240

Lys Asn Pro Asn Ala Met Leu Val Asn Leu Glu Glu Pro Leu Ala Ser
                245   250   255

Thr Tyr Gln Asp Ile Leu Tyr Gln Ala Lys Gln Asp Lys Met Thr Asn
20   260   265   270

Ala Lys Asn Arg Thr Glu Asn Ser Glu Arg Glu Arg Asp Val Tyr Glu
            275   280   285

Glu Leu Leu Thr Gln Ala Glu Ile Gln Gly Asn Ile Asn Lys Val Asn
        290   295   300

Thr Phe Ser Ala Leu Ala Asn Ile Asp Leu Ala Leu Glu Gln Gly Asp
305   310   315   320

Ala Leu Ala Leu Phe Arg Ala Leu Gln Ser Pro Ala Leu Gly Leu Arg
                  325   330   335

5   Gly Leu Gln Gln Gln Asn Ser Asp Trp Tyr Leu Lys Gln Leu Leu Ser
                  340   345   350

Asp Lys Gln Gln Lys Arg Gln Ser Gly Gln Thr Asp Pro Leu Gln Lys
        355   360   365

Glu Glu Leu Gln Ser Gly Val Asp Ala Ala Asn Ser Ala Ala Gln Gln
10   370   375   380

Tyr Gln Arg Arg Leu Ala Ala Val Ala Leu Ile Asn Ala Ala Ile Gln
385   390   395   400

Lys Gly Val Ala Glu Lys Thr Val Leu Glu Leu Met Asn Pro Glu Ala
                  405   410   415

15 Gln Leu Pro Gln Val Tyr Pro Phe Ala Ala Asp Leu Tyr Gln Lys Glu
                  420   425   430

Leu Ala Thr Leu Gln Arg Gln Ser Pro Glu His Asn Leu Thr His Pro
        435   440   445

Glu Leu Ser Val Ala Val Glu Met Leu Ser Ser Val Ala Leu Ile Asn
20   450   455   460

Arg Ala Leu Glu Ser Gly Asp Val Asn Thr Val Trp Lys Gln Leu Ser
465   470   475   480

Ser Ser Val Thr Gly Leu Thr Asn Ile Glu Glu Glu Asn Cys Gln Arg
                  485   490   495

Tyr Leu Asp Glu Leu Met Lys Leu Lys Ala Gln Ala His Ala Glu Asn
                500   505   510

Asn Glu Phe Ile Thr Trp Asn Asp Ile Gln Ala Cys Val Asp His Val
            515   520   525

5   Asn Leu Val Val Gln Glu Glu His Glu Arg Ile Leu Ala Ile Gly Leu
            530   535   540

    Ile Asn Glu Ala Leu Asp Glu Gly Asp Ala Gln Lys Thr Leu Gln Ala
    545   550   555   560

    Leu Gln Ile Pro Ala Ala Lys Leu Glu Gly Val Leu Ala Glu Val Ala
10   565   570   575

    Gln His Tyr Gln Asp Thr Leu Ile Arg Ala Lys Arg Glu Lys Ala Gln
                580   585   590

    Glu Ile Gln Asp Glu Ser Ala Val Leu Trp Leu Asp Glu Ile Gln Gly
                595   600   605

15 Gly Ile Trp Gln Ser Asn Lys Asp Thr Gln Glu Ala Gln Lys Phe Ala
            610   615   620

    Leu Gly Ile Phe Ala Ile Asn Glu Ala Val Glu Ser Gly Asp Val Gly
    625   630   635   640

    Lys Thr Leu Ser Ala Leu Arg Ser Pro Asp Val Gly Leu Tyr Gly Val
20   645   650   655

    Ile Pro Glu Cys Gly Glu Thr Tyr His Ser Asp Leu Ala Glu Ala Lys
                660   665   670

    Lys Lys Lys Leu Ala Val Gly Asp Asn Asn Ser Lys Trp Val Lys His
                675   680   685

Trp Val Lys Gly Gly Tyr Tyr Tyr His Asn Leu Glu Thr Gln Glu
　　　　690　　　　　　　695　　　　　　　　700

Gly Gly Trp Asp Glu Pro Pro Asn Phe Val Gln Asn Ser Met Gln Leu
705　　　　　　　　710　　　　　　　715　　　　　　　　720

5　Ser Arg Glu Glu Ile Gln Ser Ser Ile Ser Gly Val Thr Ala Ala Tyr
　　　　　　　725　　　　　　　　730　　　　　　　735

Asn Arg Glu Gln Leu Trp Leu Ala Asn Glu Gly Leu Ile Thr Arg Leu
　　　　740　　　　　　　　745　　　　　　　750

Gln Ala Arg Cys Arg Gly Tyr Leu Val Arg Gln Glu Phe Arg Ser Arg
10　　　　755　　　　　　　760　　　　　　　765

Met Asn Phe Leu Lys Lys Gln Ile Pro Ala Ile Thr Cys Ile Gln Ser
　　　　770　　　　　　　775　　　　　　　780

Gln Trp Arg Gly Tyr Lys Gln Lys Lys Ala Tyr Gln Asp Arg Leu Ala
785　　　　　　　　790　　　　　　　795　　　　　　　　800

15　Tyr Leu Arg Ser His Lys Asp Glu Val Val Lys Ile Gln Ser Leu Ala
　　　　　　　805　　　　　　　810　　　　　　　815

Arg Met His Gln Ala Arg Lys Arg Tyr Arg Asp Arg Leu Gln Tyr Phe
　　　　820　　　　　　　825　　　　　　　830

Arg Asp His Ile Asn Asp Ile Ile Lys Ile Gln Ala Phe Ile Arg Ala
20　　　　835　　　　　　　840　　　　　　　845

Asn Lys Ala Arg Asp Asp Tyr Lys Thr Leu Ile Asn Ala Glu Asp Pro
　　　　850　　　　　　　855　　　　　　　860

Pro Met Val Val Val Arg Lys Phe Val His Leu Leu Asp Gln Ser Asp
865　　　　　　　870　　　　　　　875　　　　　　　880

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      Gln Asp Phe Gln Glu Glu Leu Asp Leu Met Lys Met Arg Glu Glu Val

                   885               890               895

      Ile Thr Leu Ile Arg Ser Asn Gln Gln Leu Glu Asn Asp Leu Asn Leu

                   900               905               910

   5  Met Asp Ile Lys Ile Gly Leu Leu Val Lys Asn Lys Ile Thr Leu Gln

                   915               920               925

      Asp Val Val Ser His Ser Lys Lys Leu Thr Lys Lys Asn Lys Glu Gln

                   930               935               940

      Leu Ser Asp Met Met Met Ile Asn Lys Gln Lys Gly Gly Leu Lys Ala

  10  945               950               955               960

      Leu Ser Lys Glu Lys Arg Glu Lys Leu Glu Ala Tyr Gln His Leu Phe

                   965               970               975

      Tyr Leu Leu Gln Thr Asn Pro Thr Tyr Leu Ala Lys Leu Ile Phe Gln

                   980               985               990

  15  Met Pro Gln Asn Lys Ser Thr Lys  Phe Met Asp Ser Val  Ile Phe Thr

                   995              1000              1005

      Leu Tyr  Asn Tyr Ala Ser Asn  Gln Arg Glu Glu Tyr  Leu Leu Leu

                  1010              1015              1020

      Arg Leu  Phe Lys Thr Ala Leu  Gln Glu Glu Ile Lys  Ser Lys Val

  20  1025              1030              1035

      Asp Gln  Ile Gln Glu Ile Val  Thr Gly Asn Pro Thr  Val Ile Lys

                  1040              1045              1050

      Met Val  Val Ser Phe Asn Arg  Gly Ala Arg Gly Gln  Asn Ala Leu

                  1055              1060              1065
```

Arg Gln Ile Leu Ala Pro Val Val Lys Glu Ile Met Asp Asp Lys

     1070   1075   1080

Ser Leu Asn Ile Lys Thr Asp Pro Val Asp Ile Tyr Lys Ser Trp

     1085   1090   1095

5   Val Asn Gln Met Glu Ser Gln Thr Gly Glu Ala Ser Lys Leu Pro

     1100   1105   1110

Tyr Asp Val Thr Pro Glu Gln Ala Leu Ala His Glu Glu Val Lys

     1115   1120   1125

Thr Arg Leu Asp Ser Ser Ile Arg Asn Met Arg Ala Val Thr Asp

10   1130   1135   1140

Lys Phe Leu Ser Ala Ile Val Ser Ser Val Asp Lys Ile Pro Tyr

     1145   1150   1155

Gly Met Arg Phe Ile Ala Lys Val Leu Lys Asp Ser Leu His Glu

     1160   1165   1170

15 Lys Phe Pro Asp Ala Gly Glu Asp Glu Leu Leu Lys Ile Ile Gly

     1175   1180   1185

Asn Leu Leu Tyr Tyr Arg Tyr Met Asn Pro Ala Ile Val Ala Pro

     1190   1195   1200

Asp Ala Phe Asp Ile Ile Asp Leu Ser Ala Gly Gly Gln Leu Thr

20   1205   1210   1215

Thr Asp Gln Arg Arg Asn Leu Gly Ser Ile Ala Lys Met Leu Gln

     1220   1225   1230

His Ala Ala Ser Asn Lys Met Phe Leu Gly Asp Asn Ala His Leu

     1235   1240   1245

Ser Ile Ile Asn Glu Tyr Leu Ser Gln Ser Tyr Gln Lys Phe Arg

 1250   1255   1260

Arg Phe Phe Gln Thr Ala Cys Asp Val Pro Glu Leu Gln Asp Lys

 1265   1270   1275

5 Phe Asn Val Asp Glu Tyr Ser Asp Leu Val Thr Leu Thr Lys Pro

 1280   1285   1290

Val Ile Tyr Ile Ser Ile Gly Glu Ile Ile Asn Thr His Thr Leu

 1295   1300   1305

Leu Leu Asp His Gln Asp Ala Ile Ala Pro Glu His Asn Asp Pro

10   1310   1315   1320

Ile His Glu Leu Leu Asp Asp Leu Gly Glu Val Pro Thr Ile Glu

 1325   1330   1335

Ser Leu Ile Gly Glu Ser Ser Gly Asn Leu Asn Asp Pro Asn Lys

 1340   1345   1350

15 Glu Ala Leu Ala Lys Thr Glu Val Ser Leu Thr Leu Thr Asn Lys

 1355   1360   1365

Phe Asp Val Pro Gly Asp Glu Asn Ala Glu Met Asp Ala Arg Thr

 1370   1375   1380

Ile Leu Leu Asn Thr Lys Arg Leu Ile Val Asp Val Ile Arg Phe

20   1385   1390   1395

Gln Pro Gly Glu Thr Leu Thr Glu Ile Leu Glu Thr Pro Ala Thr

 1400   1405   1410

Ser Glu Gln Glu Ala Glu His Gln Arg Ala Met Gln Arg Arg Ala

 1415   1420   1425

```
     Ile Arg Asp Ala Lys Thr Pro  Asp Lys Met Lys Lys  Ser Lys Ser
         1430              1435                1440

     Val Lys Glu Asp Ser Asn Leu  Thr Leu Gln Glu Lys  Lys Glu Lys
         1445              1450                1455

5    Ile Gln Thr Gly Leu Lys Lys  Leu Thr Glu Leu Gly  Thr Val Asp
         1460              1465                1470

     Pro Lys Asn Lys Tyr Gln Glu  Leu Ile Asn Asp Ile  Ala Arg Asp
         1475              1480                1485

     Ile Arg Asn Gln Arg Arg Tyr  Arg Gln Arg Arg Lys  Ala Glu Leu
10       1490              1495                1500

     Val Lys Leu Gln Gln Thr Tyr  Ala Ala Leu Asn Ser  Lys Ala Thr
         1505              1510                1515

     Phe Tyr Gly Glu Gln Val Asp  Tyr Tyr Lys Ser Tyr  Ile Lys Thr
         1520              1525                1530

15   Cys Leu Asp Asn Leu Ala Ser  Lys Gly Lys Val Ser  Lys Lys Pro
         1535              1540                1545

     Arg Glu Met Lys Gly Lys Lys  Ser Lys Lys Ile Ser  Leu Lys Tyr
         1550              1555                1560

     Thr Ala Ala Arg Leu His Glu  Lys Gly Val Leu Leu  Glu Ile Glu
20       1565              1570                1575

     Asp Leu Gln Val Asn Gln Phe  Lys Asn Val Ile Phe  Glu Ile Ser
         1580              1585                1590

     Pro Thr Glu Glu Val Gly Asp  Phe Glu Val Lys Ala  Lys Phe Met
         1595              1600                1605
```

Gly Val   Gln Met Glu Thr Phe   Met Leu His Tyr Gln   Asp Leu Leu

    1610   1615   1620

Gln Leu   Gln Tyr Glu Gly Val   Ala Val Met Lys Leu   Phe Asp Arg

    1625   1630   1635

5   Ala Lys   Val Asn Val Asn Leu   Leu Ile Phe Leu Leu   Asn Lys Lys

        1640   1645   1650

Phe Tyr   Gly Lys

    1655

10

    <210>   26

    <211>   627

    <212>   PRT

    <213>   Homo sapiens

15 <220>

    <221>   L-plastin (Lymphocyte cytosolic protein 1)

    <222>   (1)..(627)

    <223>   Accession No. as of 09 Dec 2002: P13796

20 <400>   26

Met Ala Arg Gly Ser Val Ser Asp Glu Glu Met Met Glu Leu Arg Glu

1   5   10   15

Ala Phe Ala Lys Val Asp Thr Asp Gly Asn Gly Tyr Ile Ser Phe Asn

```
                    20                    25                    30

    Glu Leu Asn Asp Leu Phe Lys Ala Ala Cys Leu Pro Leu Pro Gly Tyr

               35                    40                    45

    Arg Val Arg Glu Ile Thr Glu Asn Leu Met Ala Thr Gly Asp Leu Asp

 5             50                    55                    60

    Gln Asp Gly Arg Ile Ser Phe Asp Glu Phe Ile Lys Ile Phe His Gly

               65                    70                    75                    80

    Leu Lys Ser Thr Asp Val Ala Lys Thr Phe Arg Lys Ala Ile Asn Lys

                         85                    90                    95

10  Lys Glu Gly Ile Cys Ala Ile Gly Gly Thr Ser Glu Gln Ser Ser Val

                        100                   105                   110

    Gly Thr Gln His Ser Tyr Ser Glu Glu Glu Lys Tyr Ala Phe Val Asn

                        115                   120                   125

    Trp Ile Asn Lys Ala Leu Glu Asn Asp Pro Asp Cys Arg His Val Ile

15             130                   135                   140

    Pro Met Asn Pro Asn Thr Asn Asp Leu Phe Asn Ala Val Gly Asp Gly

               145                   150                   155                   160

    Ile Val Leu Cys Lys Met Ile Asn Leu Ser Val Pro Asp Thr Ile Asp

                        165                   170                   175

20  Glu Arg Thr Ile Asn Lys Lys Lys Leu Thr Pro Phe Thr Ile Gln Glu

                        180                   185                   190

    Asn Leu Asn Leu Ala Leu Asn Ser Ala Ser Ala Ile Gly Cys His Val

                        195                   200                   205

    Val Asn Ile Gly Ala Glu Asp Leu Lys Glu Gly Lys Pro Tyr Leu Val
```

```
            210                215                220

    Leu Gly Leu Leu Trp Gln Val Ile Lys Ile Gly Leu Phe Ala Asp Ile

    225                230                235                240

    Glu Leu Ser Arg Asn Glu Ala Leu Ile Ala Leu Leu Arg Glu Gly Glu

5                  245                250                255

    Ser Leu Glu Asp Leu Met Lys Leu Ser Pro Glu Glu Leu Leu Leu Arg

                260                265                270

    Trp Ala Asn Tyr His Leu Glu Asn Ala Gly Cys Asn Lys Ile Gly Asn

                275                280                285

10  Phe Ser Thr Asp Ile Lys Asp Ser Lys Ala Tyr Tyr His Leu Leu Glu

                290                295                300

    Gln Val Ala Pro Lys Gly Asp Glu Glu Gly Val Pro Ala Val Val Ile

    305                310                315                320

    Asp Met Ser Gly Leu Arg Glu Lys Asp Asp Ile Gln Arg Ala Glu Cys

15                 325                330                335

    Met Leu Gln Gln Ala Glu Arg Leu Gly Cys Arg Gln Phe Val Thr Ala

                340                345                350

    Thr Asp Val Val Arg Gly Asn Pro Lys Leu Asn Leu Ala Phe Ile Ala

                355                360                365

20  Asn Leu Phe Asn Arg Tyr Pro Ala Leu His Lys Pro Glu Asn Gln Asp

                370                375                380

    Ile Asp Trp Gly Ala Leu Glu Gly Glu Thr Arg Glu Glu Arg Thr Phe

    385                390                395                400

    Arg Asn Trp Met Asn Ser Leu Gly Val Asn Pro Arg Val Asn His Leu
```

```
                      405                    410                    415

    Tyr Ser Asp Leu Ser Asp Ala Leu Val Ile Phe Gln Leu Tyr Glu Lys

                 420                    425                    430

    Ile Lys Val Pro Val Asp Trp Asn Arg Val Asn Lys Pro Pro Tyr Pro

 5           435                    440                    445

    Lys Leu Gly Gly Asn Met Lys Lys Leu Glu Asn Cys Asn Tyr Ala Val

             450                    455                    460

    Glu Leu Gly Lys Asn Gln Ala Lys Phe Ser Leu Val Gly Ile Gly Gly

        465                    470                    475                    480

10  Gln Asp Leu Asn Glu Gly Asn Arg Thr Leu Thr Leu Ala Leu Ile Trp

                 485                    490                    495

    Gln Leu Met Arg Arg Tyr Thr Leu Asn Ile Leu Glu Glu Ile Gly Gly

                 500                    505                    510

    Gly Gln Lys Val Asn Asp Asp Ile Ile Val Asn Trp Val Asn Glu Thr

15           515                    520                    525

    Leu Arg Glu Ala Glu Lys Ser Ser Ser Ile Ser Ser Phe Lys Asp Pro

             530                    535                    540

    Lys Ile Ser Thr Ser Leu Pro Val Leu Asp Leu Ile Asp Ala Ile Gln

        545                    550                    555                    560

20  Pro Gly Ser Ile Asn Tyr Asp Leu Leu Lys Thr Glu Asn Leu Asn Asp

                 565                    570                    575

    Asp Glu Lys Leu Asn Asn Ala Lys Tyr Ala Ile Ser Met Ala Arg Lys

                 580                    585                    590

    Ile Gly Ala Arg Val Tyr Ala Leu Pro Glu Asp Leu Val Glu Val Asn
```

                  595   600   605

    Pro Lys Met Val Met Thr Val Phe Ala Cys Leu Met Gly Lys Gly Met

             610   615   620

    Lys Arg Val

 5   625

    <210>   27

    <211>   216

10 <212>   PRT

    <213>   Homo sapiens

    <220>

    <221>   GTP-binding nuclear protein RAN

    <222>   (1)..(216)

15 <223>   Accession No. as of 09 Dec 2002: P17080

    <400>   27

    Met Ala Ala Gln Gly Glu Pro Gln Val Gln Phe Lys Leu Val Leu Val

    1   5   10   15

20 Gly Asp Gly Gly Thr Gly Lys Thr Thr Phe Val Lys Arg His Leu Thr

                  20   25   30

    Gly Glu Phe Glu Lys Lys Tyr Val Ala Thr Leu Gly Val Glu Val His

             35   40   45

    Pro Leu Val Phe His Thr Asn Arg Gly Pro Ile Lys Phe Asn Val Trp

```
              50                    55                    60
      Asp Thr Ala Gly Gln Glu Lys Phe Gly Gly Leu Arg Asp Gly Tyr Tyr
              65                    70                    75                80
      Ile Gln Ala Gln Cys Ala Ile Ile Met Phe Asp Val Thr Ser Arg Val
5                         85                    90                    95
      Thr Tyr Lys Asn Val Pro Asn Trp His Arg Asp Leu Val Arg Val Cys
                      100                   105                   110
      Glu Asn Ile Pro Ile Val Leu Cys Gly Asn Lys Val Asp Ile Lys Asp
                  115                   120                   125
10    Arg Lys Val Lys Ala Lys Ser Ile Val Phe His Arg Lys Lys Asn Leu
              130                   135                   140
      Gln Tyr Tyr Asp Ile Ser Ala Lys Ser Asn Tyr Asn Phe Glu Lys Pro
      145                   150                   155                   160
      Phe Leu Trp Leu Ala Arg Lys Leu Ile Gly Asp Pro Asn Leu Glu Phe
15                        165                   170                   175
      Val Ala Met Pro Ala Leu Ala Pro Pro Glu Val Val Met Asp Pro Ala
                      180                   185                   190
      Leu Ala Ala Gln Tyr Glu His Asp Leu Glu Val Ala Gln Thr Thr Ala
                  195                   200                   205
20    Leu Pro Asp Glu Asp Asp Leu
              210                   215
```

<210>   28

<211> 463

<212> PRT

<213> Homo sapiens

<220>

5 <221> Heterogeneous nuclear ribonucleoprotein K

<222> (1)..(463)

<223> Accession No. as of 09 Dec 2002: Q07244

<400> 28

10 Met Glu Thr Glu Gln Pro Glu Glu Thr Phe Pro Asn Thr Glu Thr Asn

    1   5   10   15

    Gly Glu Phe Gly Lys Arg Pro Ala Glu Asp Met Glu Glu Glu Gln Ala

                    20   25   30

    Phe Lys Arg Ser Arg Asn Thr Asp Glu Met Val Glu Leu Arg Ile Leu

15   35   40   45

    Leu Gln Ser Lys Asn Ala Gly Ala Val Ile Gly Lys Gly Gly Lys Asn

                50   55   60

    Ile Lys Ala Leu Arg Thr Asp Tyr Asn Ala Ser Val Ser Val Pro Asp

    65   70   75   80

20 Ser Ser Gly Pro Glu Arg Ile Leu Ser Ile Ser Ala Asp Ile Glu Thr

                    85   90   95

    Ile Gly Glu Ile Leu Lys Lys Ile Ile Pro Thr Leu Glu Glu Gly Leu

                    100   105   110

    Gln Leu Pro Ser Pro Thr Ala Thr Ser Gln Leu Pro Leu Glu Ser Asp

```
              115                    120                    125

      Ala Val Glu Cys Leu Asn Tyr Gln His Tyr Lys Gly Ser Asp Phe Asp

              130                    135                    140

      Cys Glu Leu Arg Leu Leu Ile His Gln Ser Leu Ala Gly Gly Ile Ile

   5  145                    150                    155                    160

      Gly Val Lys Gly Ala Lys Ile Lys Glu Leu Arg Glu Asn Thr Gln Thr

                     165                    170                    175

      Thr Ile Lys Leu Phe Gln Glu Cys Cys Pro His Ser Thr Asp Arg Val

                     180                    185                    190

  10  Val Leu Ile Gly Gly Lys Pro Asp Arg Val Val Glu Cys Ile Lys Ile

                     195                    200                    205

      Ile Leu Asp Leu Ile Ser Glu Ser Pro Ile Lys Gly Arg Ala Gln Pro

                     210                    215                    220

      Tyr Asp Pro Asn Phe Tyr Asp Glu Thr Tyr Asp Tyr Gly Gly Phe Thr

  15  225                    230                    235                    240

      Met Met Phe Asp Asp Arg Arg Gly Arg Pro Val Gly Phe Pro Met Arg

                     245                    250                    255

      Gly Arg Gly Gly Phe Asp Arg Met Pro Pro Gly Arg Gly Gly Arg Pro

                     260                    265                    270

  20  Met Pro Pro Ser Arg Arg Asp Tyr Asp Asp Met Ser Pro Arg Arg Gly

                     275                    280                    285

      Pro Pro Pro Pro Pro Pro Gly Arg Gly Gly Arg Gly Gly Ser Arg Ala

                     290                    295                    300

      Arg Asn Leu Pro Leu Pro Pro Pro Pro Pro Pro Arg Gly Gly Asp Leu
```

```
        305                    310                    315                    320
    Met Ala Tyr Asp Arg Arg Gly Arg Pro Gly Asp Arg Tyr Asp Gly Met

                    325                    330                    335
    Val Gly Phe Ser Ala Asp Glu Thr Trp Asp Ser Ala Ile Asp Thr Trp

5                   340                    345                    350
    Ser Pro Ser Glu Trp Gln Met Ala Tyr Glu Pro Gln Gly Gly Ser Gly

                355                    360                    365
    Tyr Asp Tyr Ser Tyr Ala Gly Gly Arg Gly Ser Tyr Gly Asp Leu Gly

            370                    375                    380
10  Gly Pro Ile Ile Thr Thr Gln Val Thr Ile Pro Lys Asp Leu Ala Gly

    385                    390                    395                    400
    Ser Ile Ile Gly Lys Gly Gly Gln Arg Ile Lys Gln Ile Arg His Glu

                    405                    410                    415
    Ser Gly Ala Ser Ile Lys Ile Asp Glu Pro Leu Glu Gly Ser Glu Asp

15                  420                    425                    430
    Arg Ile Ile Thr Ile Thr Gly Thr Gln Asp Gln Ile Gln Asn Ala Gln

            435                    440                    445
    Tyr Leu Leu Gln Asn Ser Val Lys Gln Tyr Ser Gly Lys Phe Phe

        450                    455                    460
20
```

```
    <210>   29

    <211>   172

    <212>   PRT
```

<213>   Homo sapiens

<220>

<221>   Translationally controlled tumor protein (TCTP)

<222>   (1)..(172)

5   <223>   Accession No. as of 09 Dec 2002: P13693

<400>   29

Met Ile Ile Tyr Arg Asp Leu Ile Ser His Asp Glu Met Phe Ser Asp

1   5   10   15

10   Ile Tyr Lys Ile Arg Glu Ile Ala Asp Gly Leu Cys Leu Glu Val Glu

                 20   25   30

Gly Lys Met Val Ser Arg Thr Glu Gly Asn Ile Asp Asp Ser Leu Ile

                 35   40   45

Gly Gly Asn Ala Ser Ala Glu Gly Pro Glu Gly Glu Gly Thr Glu Ser

15   50   55   60

Thr Val Ile Thr Gly Val Asp Ile Val Met Asn His His Leu Gln Glu

65   70   75   80

Thr Ser Phe Thr Lys Glu Ala Tyr Lys Lys Tyr Ile Lys Asp Tyr Met

                 85   90   95

20   Lys Ser Ile Lys Gly Lys Leu Glu Glu Gln Arg Pro Glu Arg Val Lys

                 100   105   110

Pro Phe Met Thr Gly Ala Ala Glu Gln Ile Lys His Ile Leu Ala Asn

                 115   120   125

Phe Lys Asn Tyr Gln Phe Phe Ile Gly Glu Asn Met Asn Pro Asp Gly

          130   135   140

    Met Val Ala Leu Leu Asp Tyr Arg Glu Asp Gly Val Thr Pro Tyr Met

        145   150   155   160

    Ile Phe Phe Lys Asp Gly Leu Glu Met Glu Lys Cys

5   165   170

    <210> 30

    <211> 284

10 <212> PRT

    <213> Homo sapiens

    <220>

    <221> Tropomyosin 1 alpha chain

    <222> (1)..(284)

15 <223> Accession No. as of 06 Dec 2002: P09493

    <400> 30

    Met Asp Ala Ile Lys Lys Lys Met Gln Met Leu Lys Leu Asp Lys Glu

    1   5   10   15

20 Asn Ala Leu Asp Arg Ala Glu Gln Ala Glu Ala Asp Lys Lys Ala Ala

                20   25   30

    Glu Asp Arg Ser Lys Gln Leu Glu Asp Glu Leu Val Ser Leu Gln Lys

            35   40   45

    Lys Leu Lys Gly Thr Glu Asp Glu Leu Asp Lys Tyr Ser Glu Ala Leu

                  50   55   60

        Lys Asp Ala Gln Glu Lys Leu Glu Leu Ala Glu Lys Lys Ala Thr Asp

              65   70   75   80

        Ala Glu Ala Asp Val Ala Ser Leu Asn Arg Arg Ile Gln Leu Val Glu

    5   85   90   95

        Glu Glu Leu Asp Arg Ala Gln Glu Arg Leu Ala Thr Ala Leu Gln Lys

                      100   105   110

        Leu Glu Glu Ala Glu Lys Ala Ala Asp Glu Ser Glu Arg Gly Met Lys

                  115   120   125

   10   Val Ile Glu Ser Arg Ala Gln Lys Asp Glu Glu Lys Met Glu Ile Gln

                  130   135   140

        Glu Ile Gln Leu Lys Glu Ala Lys His Ile Ala Glu Asp Ala Asp Arg

              145   150   155   160

        Lys Tyr Glu Glu Val Ala Arg Lys Leu Val Ile Ile Glu Ser Asp Leu

   15   165   170   175

        Glu Arg Ala Glu Glu Arg Ala Glu Leu Ser Glu Gly Lys Cys Ala Glu

                      180   185   190

        Leu Glu Glu Glu Leu Lys Thr Val Thr Asn Asn Leu Lys Ser Leu Glu

                  195   200   205

   20   Ala Gln Ala Glu Lys Tyr Ser Gln Lys Glu Asp Arg Tyr Glu Glu Glu

                  210   215   220

        Ile Lys Val Leu Ser Asp Lys Leu Lys Glu Ala Glu Thr Arg Ala Glu

              225   230   235   240

        Phe Ala Glu Arg Ser Val Thr Lys Leu Glu Lys Ser Ile Asp Asp Leu

                    245   250   255

    Glu Asp Glu Leu Tyr Ala Gln Lys Leu Lys Tyr Lys Ala Ile Ser Glu

                        260   265   270

    Glu Leu Asp His Ala Leu Asn Asp Met Thr Ser Ile

5   275   280

        <210>   31

        <211>   482

10   <212>   PRT

        <213>   Homo sapiens

        <220>

        <221>   Thymidine phosphorylase precursor

        <222>   (1)..(482)

15   <223>   Accession No. as of 09 Dec 2002: P19971

        <400>   31

    Met Ala Ala Leu Met Thr Pro Gly Thr Gly Ala Pro Pro Ala Pro Gly

    1   5   10   15

20 Asp Phe Ser Gly Glu Gly Ser Gln Gly Leu Pro Asp Pro Ser Pro Glu

                        20   25   30

    Pro Lys Gln Leu Pro Glu Leu Ile Arg Met Lys Arg Asp Gly Gly Arg

                    35   40   45

    Leu Ser Glu Ala Asp Ile Arg Gly Phe Val Ala Ala Val Val Asn Gly

```
                50                     55                     60

        Ser Ala Gln Gly Ala Gln Ile Gly Ala Met Leu Met Ala Ile Arg Leu

                65                     70                     75                     80

        Arg Gly Met Asp Leu Glu Glu Thr Ser Val Leu Thr Gln Ala Leu Ala

  5                             85                     90                     95

        Gln Ser Gly Gln Gln Leu Glu Trp Pro Glu Ala Trp Arg Gln Gln Leu

                        100                    105                    110

        Val Asp Lys His Ser Thr Gly Gly Val Gly Asp Lys Val Ser Leu Val

                        115                    120                    125

 10     Leu Ala Pro Ala Leu Ala Ala Cys Gly Cys Lys Val Pro Met Ile Ser

                        130                    135                    140

        Gly Arg Gly Leu Gly His Thr Gly Gly Thr Leu Asp Lys Leu Glu Ser

                145                    150                    155                    160

        Ile Pro Gly Phe Asn Val Ile Gln Ser Pro Glu Gln Met Gln Val Leu

 15                             165                    170                    175

        Leu Asp Gln Ala Gly Cys Cys Ile Val Gly Gln Ser Glu Gln Leu Val

                        180                    185                    190

        Pro Ala Asp Gly Ile Leu Tyr Ala Ala Arg Asp Val Thr Ala Thr Val

                        195                    200                    205

 20     Asp Ser Leu Pro Leu Ile Thr Ala Ser Ile Leu Ser Lys Lys Leu Val

                        210                    215                    220

        Glu Gly Leu Ser Ala Leu Val Val Asp Val Lys Phe Gly Gly Ala Ala

                225                    230                    235                    240

        Val Phe Pro Asn Gln Glu Gln Ala Arg Glu Leu Ala Lys Thr Leu Val
```

```
                       245                  250                  255

        Gly Val Gly Ala Ser Leu Gly Leu Arg Val Ala Ala Ala Leu Thr Ala

                            260                  265                  270

        Met Asp Lys Pro Leu Gly Arg Cys Val Gly His Ala Leu Glu Val Glu

     5            275                  280                  285

        Glu Ala Leu Leu Cys Met Asp Gly Ala Gly Pro Pro Asp Leu Arg Asp

                       290                  295                  300

        Leu Val Thr Thr Leu Gly Gly Ala Leu Leu Trp Leu Ser Gly His Ala

                 305                  310                  315                  320

    10  Gly Thr Gln Ala Gln Gly Ala Ala Arg Val Ala Ala Ala Leu Asp Asp

                            325                  330                  335

        Gly Ser Ala Leu Gly Arg Phe Glu Arg Met Leu Ala Ala Gln Gly Val

                            340                  345                  350

        Asp Pro Gly Leu Ala Arg Ala Leu Cys Ser Gly Ser Pro Ala Glu Arg

    15            355                  360                  365

        Arg Gln Leu Leu Pro Arg Ala Arg Glu Gln Glu Glu Leu Leu Ala Pro

                       370                  375                  380

        Ala Asp Gly Thr Val Glu Leu Val Arg Ala Leu Pro Leu Ala Leu Val

                 385                  390                  395                  400

    20  Leu His Glu Leu Gly Ala Gly Arg Ser Arg Ala Gly Glu Pro Leu Arg

                            405                  410                  415

        Leu Gly Val Gly Ala Glu Leu Leu Val Asp Val Gly Gln Arg Leu Arg

                            420                  425                  430

        Arg Gly Thr Pro Trp Leu Arg Val His Arg Asp Gly Pro Ala Leu Ser
```

            435   440   445

    Gly Pro Gln Ser Arg Ala Leu Gln Glu Ala Leu Val Leu Ser Asp Arg

            450   455   460

    Ala Pro Phe Ala Ala Pro Leu Pro Phe Ala Glu Leu Val Leu Pro Pro

5   465   470   475   480

    Gln Gln

10 <210>   32

    <211>   488

    <212>   PRT

    <213>   Homo sapiens

    <220>

15 <221>   Cytosol aminopeptidase

    <222>   (1)..(488)

    <223>   Accession No. as of 09 Dec 2002: P28838

    <400>   32

20 Met Thr Lys Gly Leu Val Leu Gly Ile Tyr Ser Lys Glu Lys Glu Asp

    1   5   10   15

    Asp Val Pro Gln Phe Thr Ser Ala Gly Glu Asn Phe Asp Lys Leu Leu

                20   25   30

    Ala Gly Lys Leu Arg Glu Thr Leu Asn Ile Ser Gly Pro Pro Leu Lys

                35   40   45

      Ala Gly Lys Thr Arg Thr Phe Tyr Gly Leu His Gln Asp Phe Pro Ser

                50   55   60

      Val Val Leu Val Gly Leu Gly Lys Lys Ala Ala Gly Ile Asp Glu Gln

5   65   70   75   80

      Glu Asn Trp His Glu Gly Lys Glu Asn Ile Arg Ala Ala Val Ala Ala

                            85   90   95

      Gly Cys Arg Gln Ile Gln Asp Leu Glu Leu Ser Ser Val Glu Val Asp

                        100   105   110

10   Pro Cys Gly Asp Ala Gln Ala Ala Ala Glu Gly Ala Val Leu Gly Leu

                    115   120   125

      Tyr Glu Tyr Asp Asp Leu Lys Gln Lys Lys Met Ala Val Ser Ala

                    130   135   140

      Lys Leu Tyr Gly Ser Gly Asp Gln Glu Ala Trp Gln Lys Gly Val Leu

15   145   150   155   160

      Phe Ala Ser Gly Gln Asn Leu Ala Arg Gln Leu Met Glu Thr Pro Ala

                        165   170   175

      Asn Glu Met Thr Pro Thr Arg Phe Ala Glu Ile Ile Glu Lys Asn Leu

                        180   185   190

20   Lys Ser Ala Ser Ser Lys Thr Glu Val His Ile Arg Pro Lys Ser Trp

                    195   200   205

      Ile Glu Glu Gln Ala Met Gly Ser Phe Leu Ser Val Ala Lys Gly Ser

                    210   215   220

      Asp Glu Pro Pro Val Phe Leu Glu Ile His Tyr Lys Gly Ser Pro Asn

```
        225                 230                 235                 240
```

Ala Asn Glu Pro Pro Leu Val Phe Val Gly Lys Gly Ile Thr Phe Asp

```
                245                 250                 255
```

Ser Gly Gly Ile Ser Ile Lys Ala Ser Ala Asn Met Asp Leu Met Arg

```
5               260                 265                 270
```

Ala Asp Met Gly Gly Ala Ala Thr Ile Cys Ser Ala Ile Val Ser Ala

```
                275                 280                 285
```

Ala Lys Leu Asn Leu Pro Ile Asn Ile Ile Gly Leu Ala Pro Leu Cys

```
            290                 295                 300
```

10 Glu Asn Met Pro Ser Gly Lys Ala Asn Lys Pro Gly Asp Val Val Arg

```
    305                 310                 315                 320
```

Ala Lys Asn Gly Lys Thr Ile Gln Val Asp Asn Thr Asp Ala Glu Gly

```
                325                 330                 335
```

Arg Leu Ile Leu Ala Asp Ala Leu Cys Tyr Ala His Thr Phe Asn Pro

```
15              340                 345                 350
```

Lys Val Ile Leu Asn Ala Ala Thr Leu Thr Gly Ala Met Asp Val Ala

```
            355                 360                 365
```

Leu Gly Ser Gly Ala Thr Gly Val Phe Thr Asn Ser Ser Trp Leu Trp

```
        370                 375                 380
```

20 Asn Lys Leu Phe Glu Ala Ser Ile Glu Thr Gly Asp Arg Val Trp Arg

```
    385                 390                 395                 400
```

Met Pro Leu Phe Glu His Tyr Thr Arg Gln Val Val Asp Cys Gln Leu

```
            405                 410                 415
```

Ala Asp Val Asn Asn Ile Gly Lys Tyr Arg Ser Ala Gly Ala Cys Thr

	420					425					430			

Ala Ala Ala Phe Leu Lys Glu Phe Val Thr His Pro Lys Trp Ala His

	435					440					445			

Leu Asp Ile Ala Gly Val Met Thr Asn Lys Asp Glu Val Pro Tyr Leu

5   450   455   460

Arg Lys Gly Met Thr Gly Arg Pro Thr Arg Thr Leu Ile Glu Phe Leu

465   470   475   480

Leu Arg Phe Ser Gln Asp Asn Ala

              485

10

<210>   33

<211>   400

<212>   PRT

15   <213>   Homo sapiens

<220>

<221>   Keratin, type I cytoskeletal 19

<222>   (1)..(400)

<223>   Accession No. as of 09 Dec 2002 : P08727

20

<400>   33

Met Thr Ser Tyr Ser Tyr Arg Gln Ser Ser Ala Thr Ser Ser Phe Gly

1   5   10   15

Gly Leu Gly Gly Gly Ser Val Arg Phe Gly Pro Gly Val Ala Phe Arg
                20   25   30

Ala Pro Ser Ile His Gly Gly Ser Gly Gly Arg Gly Val Ser Val Ser
                35   40   45

5   Ser Ala Arg Phe Val Ser Ser Ser Ser Gly Gly Tyr Gly Gly Gly
                50   55   60

Tyr Gly Gly Val Leu Thr Ala Ser Asp Gly Leu Leu Ala Gly Asn Glu
    65   70   75   80

Lys Leu Thr Met Gln Asn Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp
10   85   90   95

Lys Val Arg Ala Leu Glu Ala Ala Asn Gly Glu Leu Glu Val Lys Ile
                100   105   110

Arg Asp Trp Tyr Gln Lys Gln Gly Pro Gly Pro Ser Arg Asp Tyr Ser
                115   120   125

15 His Tyr Tyr Thr Thr Ile Gln Asp Leu Arg Asp Lys Ile Leu Gly Ala
                130   135   140

Thr Ile Glu Asn Ser Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu
    145   150   155   160

Ala Ala Asp Asp Phe Arg Thr Lys Phe Glu Thr Glu Gln Ala Leu Arg
20   165   170   175

Met Ser Val Glu Ala Asp Ile Asn Gly Leu Arg Arg Val Leu Asp Glu
                180   185   190

Leu Thr Leu Ala Arg Thr Asp Leu Glu Met Gln Ile Glu Gly Leu Lys
                195   200   205

Glu Glu Leu Ala Tyr Leu Lys Lys Asn His Glu Glu Glu Ile Ser Thr

210 215 220

Leu Arg Gly Gln Val Gly Gly Gln Val Ser Val Glu Val Asp Ser Ala

225 230 235 240

5 Pro Gly Thr Asp Leu Ala Lys Ile Leu Ser Asp Met Arg Ser Gln Tyr

245 250 255

Glu Val Met Ala Glu Gln Asn Arg Lys Asp Ala Glu Ala Trp Phe Thr

260 265 270

Ser Arg Thr Glu Glu Leu Asn Arg Glu Val Ala Gly His Thr Glu Gln

10 275 280 285

Leu Gln Met Ser Arg Ser Glu Val Thr Asp Leu Arg Arg Thr Leu Gln

290 295 300

Gly Leu Glu Ile Glu Leu Gln Ser Gln Leu Ser Met Lys Ala Ala Leu

305 310 315 320

15 Glu Asp Thr Leu Ala Glu Thr Glu Ala Arg Phe Gly Ala Gln Leu Ala

325 330 335

His Ile Gln Ala Leu Ile Ser Gly Ile Glu Ala Gln Leu Ala Asp Val

340 345 350

Arg Ala Asp Ser Glu Arg Gln Asn Gln Glu Tyr Gln Arg Leu Met Asp

20 355 360 365

Ile Lys Ser Arg Leu Glu Gln Glu Ile Ala Thr Tyr Arg Ser Leu Leu

370 375 380

Glu Gly Gln Glu Asp His Tyr Asn Asn Leu Ser Ala Ser Lys Val Leu

385 390 395 400

<210> 34

<211> 325

5   <212> PRT

<213> Homo sapiens

<220>

<221> Alcohol dehydrogenase [NADP+]

<222> (1)..(325)

10 <223> Accession No. as of 09 Dec 2002: P14550

<400> 34

```
    Met Ala Ala Ser Cys Val Leu Leu His Thr Gly Gln Lys Met Pro Leu
    1               5                   10                  15

15  Ile Gly Leu Gly Thr Trp Lys Ser Glu Pro Gly Gln Val Lys Ala Ala
                    20                  25                  30

    Val Lys Tyr Ala Leu Ser Val Gly Tyr Arg His Ile Asp Cys Ala Ala
                    35                  40                  45

    Ile Tyr Gly Asn Glu Pro Glu Ile Gly Glu Ala Leu Lys Glu Asp Val
20      50                  55                  60

    Gly Pro Gly Lys Ala Val Pro Arg Glu Glu Leu Phe Val Thr Ser Lys
        65                  70                  75                  80

    Leu Trp Asn Thr Lys His His Pro Glu Asp Val Glu Pro Ala Leu Arg
                    85                  90                  95
```

```
      Lys Thr Leu Ala Asp Leu Gln Leu Glu Tyr Leu Asp Leu Tyr Leu Met
                100                 105                 110

      His Trp Pro Tyr Ala Phe Glu Arg Gly Asp Asn Pro Phe Pro Lys Asn
                115                 120                 125

   5  Ala Asp Gly Thr Ile Cys Tyr Asp Ser Thr His Tyr Lys Glu Thr Trp
                130                 135                 140

      Lys Ala Leu Glu Ala Leu Val Ala Lys Gly Leu Val Gln Ala Leu Gly
                145                 150                 155                 160

      Leu Ser Asn Phe Asn Ser Arg Gln Ile Asp Asp Ile Leu Ser Val Ala
  10                165                 170                 175

      Ser Val Arg Pro Ala Val Leu Gln Val Glu Cys His Pro Tyr Leu Ala
                    180                 185                 190

      Gln Asn Glu Leu Ile Ala His Cys Gln Ala Arg Gly Leu Glu Val Thr
                195                 200                 205

  15  Ala Tyr Ser Pro Leu Gly Ser Ser Asp Arg Ala Trp Arg Asp Pro Asp
                210                 215                 220

      Glu Pro Val Leu Leu Glu Glu Pro Val Val Leu Ala Leu Ala Glu Lys
                225                 230                 235                 240

      Tyr Gly Arg Ser Pro Ala Gln Ile Leu Leu Arg Trp Gln Val Gln Arg
  20                245                 250                 255

      Lys Val Ile Cys Ile Pro Lys Ser Ile Thr Pro Ser Arg Ile Leu Gln
                260                 265                 270

      Asn Ile Lys Val Phe Asp Phe Thr Phe Ser Pro Glu Glu Met Lys Gln
                275                 280                 285
```

Leu Asn Ala Leu Asn Lys Asn Trp Arg Tyr Ile Val Pro Met Leu Thr

        290   295   300

Val Asp Gly Lys Arg Val Pro Arg Asp Ala Gly His Pro Leu Tyr Pro

    305   310   315   320

5 Phe Asn Asp Pro Tyr

                    325

    <210>   35

10 <211>   270

    <212>   PRT

    <213>   Homo sapiens

    <220>

    <221>   Elastase IIIA precursor

15 <222>   (1)..(270)

    <223>   Accession No. as of 09 Dec 2002: P09093

    <400>   35

    Met Met Leu Arg Leu Leu Ser Ser Leu Leu Leu Val Ala Val Ala Ser

20 1   5   10   15

    Gly Tyr Gly Pro Pro Ser Ser His Ser Ser Ser Arg Val Val His Gly

                    20   25   30

    Glu Asp Ala Val Pro Tyr Ser Trp Pro Trp Gln Val Ser Leu Gln Tyr

                    35   40   45

Glu Lys Ser Gly Ser Phe Tyr His Thr Cys Gly Gly Ser Leu Ile Ala
         50   55   60

Pro Asp Trp Val Val Thr Ala Gly His Cys Ile Ser Arg Asp Leu Thr
    65   70   75   80

5   Tyr Gln Val Val Leu Gly Glu Tyr Asn Leu Ala Val Lys Glu Gly Pro
                        85   90   95

Glu Gln Val Ile Pro Ile Asn Ser Glu Glu Leu Phe Val His Pro Leu
            100   105   110

Trp Asn Arg Ser Cys Val Ala Cys Gly Asn Asp Ile Ala Leu Ile Lys
10   115   120   125

Leu Ser Arg Ser Ala Gln Leu Gly Asp Ala Val Gln Leu Ala Ser Leu
            130   135   140

Pro Pro Ala Gly Asp Ile Leu Pro Asn Lys Thr Pro Cys Tyr Ile Thr
    145   150   155   160

15   Gly Trp Gly Arg Leu Tyr Thr Asn Gly Pro Leu Pro Asp Lys Leu Gln
                        165   170   175

Gln Ala Arg Leu Pro Val Val Asp Tyr Lys His Cys Ser Arg Trp Asn
            180   185   190

Trp Trp Gly Ser Thr Val Lys Lys Thr Met Val Cys Ala Gly Gly Tyr
20   195   200   205

Ile Arg Ser Gly Cys Asn Gly Asp Ser Gly Gly Pro Leu Asn Cys Pro
            210   215   220

Thr Glu Asp Gly Gly Trp Gln Val His Gly Val Thr Ser Phe Val Ser
    225   230   235   240

```
Gly Phe Gly Cys Asn Phe Ile Trp Lys Pro Thr Val Phe Thr Arg Val

                245                 250                 255

Ser Ala Phe Ile Asp Trp Ile Glu Glu Thr Ile Ala Ser His

                260                 265                 270
```

5

<210> 36

<211> 509

<212> PRT

10 <213> Homo sapiens

<220>

<221> Dihydrolipoamide dehydrogenase, mitochondrial precursor

<222> (1)..(509)

<223> Accession No. as of 09 Dec 2002: P09622

15 <400> 36


```
Met Gln Ser Trp Ser Arg Val Tyr Cys Ser Leu Ala Lys Arg Gly His

1               5                   10                  15

Phe Asn Arg Ile Ser His Gly Leu Gln Gly Leu Ser Ala Val Pro Leu

20              20                  25                  30

Arg Thr Tyr Ala Asp Gln Pro Ile Asp Ala Asp Val Thr Val Ile Gly

                35                  40                  45

Ser Gly Pro Gly Gly Tyr Val Ala Ala Ile Lys Ala Ala Gln Leu Gly

                50                  55                  60
```

Phe Lys Thr Val Cys Ile Glu Lys Asn Glu Thr Leu Gly Gly Thr Cys
    65   70   75   80

Leu Asn Val Gly Cys Ile Pro Ser Lys Ala Leu Leu Asn Asn Ser His
            85   90   95

5 Tyr Tyr His Met Ala His Gly Thr Asp Phe Ala Ser Arg Gly Ile Glu
            100   105   110

Met Ser Glu Val Arg Leu Asn Leu Asp Lys Met Met Glu Gln Lys Ser
            115   120   125

Thr Ala Val Lys Ala Leu Thr Gly Gly Ile Ala His Leu Phe Lys Gln
10   130   135   140

Asn Lys Val Val His Val Asn Gly Tyr Gly Lys Ile Thr Gly Lys Asn
   145   150   155   160

Gln Val Thr Ala Thr Lys Ala Asp Gly Gly Thr Gln Val Ile Asp Thr
            165   170   175

15 Lys Asn Ile Leu Ile Ala Thr Gly Ser Glu Val Thr Pro Phe Pro Gly
            180   185   190

Ile Thr Ile Asp Glu Asp Thr Ile Val Ser Ser Thr Gly Ala Leu Ser
            195   200   205

Leu Lys Lys Val Pro Glu Lys Met Val Val Ile Gly Ala Gly Val Ile
20   210   215   220

Gly Val Glu Leu Gly Ser Val Trp Gln Arg Leu Gly Ala Asp Val Thr
   225   230   235   240

Ala Val Glu Phe Leu Gly His Val Gly Gly Val Gly Ile Asp Met Glu
            245   250   255

Ile Ser Lys Asn Phe Gln Arg Ile Leu Gln Lys Gln Gly Phe Lys Phe

          260   265   270

Lys Leu Asn Thr Lys Val Thr Gly Ala Thr Lys Lys Ser Asp Gly Lys

          275   280   285

5   Ile Asp Val Ser Ile Glu Ala Ala Ser Gly Gly Lys Ala Glu Val Ile

          290   295   300

Thr Cys Asp Val Leu Leu Val Cys Ile Gly Arg Arg Pro Phe Thr Lys

305   310   315   320

Asn Leu Gly Leu Glu Glu Leu Gly Ile Glu Leu Asp Pro Arg Gly Arg

10   325   330   335

Ile Pro Val Asn Thr Arg Phe Gln Thr Lys Ile Pro Asn Ile Tyr Ala

          340   345   350

Ile Gly Asp Val Val Ala Gly Pro Met Leu Ala His Lys Ala Glu Asp

          355   360   365

15 Glu Gly Ile Ile Cys Val Glu Gly Met Ala Gly Gly Ala Val His Ile

          370   375   380

Asp Tyr Asn Cys Val Pro Ser Val Ile Tyr Thr His Pro Glu Val Ala

385   390   395   400

Trp Val Gly Lys Ser Glu Glu Gln Leu Lys Glu Glu Gly Ile Glu Tyr

20   405   410   415

Lys Val Gly Lys Phe Pro Phe Ala Ala Asn Ser Arg Ala Lys Thr Asn

          420   425   430

Ala Asp Thr Asp Gly Met Val Lys Ile Leu Gly Gln Lys Ser Thr Asp

          435   440   445

Arg Val Leu Gly Ala His Ile Leu Gly Pro Gly Ala Gly Glu Met Val

450   455   460

Asn Glu Ala Ala Leu Ala Leu Glu Tyr Gly Ala Ser Cys Glu Asp Ile

465   470   475   480

5   Ala Arg Val Cys His Ala His Pro Thr Leu Ser Glu Ala Phe Arg Glu

485   490   495

Ala Asn Leu Ala Ala Ser Phe Gly Lys Ser Ile Asn Phe

500   505

10

<210>   37

<211>   290

<212>   PRT

<213>   Homo sapiens

15 <220>

<221>   Enoyl-CoA hydratase, mitochondrial precursor

<222>   (1)..(290)

<223>   Accession No. as of 09 Dec 2002: P30084

<400>   37

20

Met Ala Ala Leu Arg Val Leu Leu Ser Cys Ala Arg Gly Pro Leu Arg

1   5   10   15

Pro Pro Val Arg Cys Pro Ala Trp Arg Pro Phe Ala Ser Gly Ala Asn

20   25   30

Phe Glu Tyr Ile Ile Ala Glu Lys Arg Gly Lys Asn Asn Thr Val Gly
            35   40   45

Leu Ile Gln Leu Asn Arg Pro Lys Ala Leu Asn Ala Leu Cys Asp Gly
            50   55   60

5 Leu Ile Asp Glu Leu Asn Gln Ala Leu Lys Ile Phe Glu Glu Asp Pro
            65   70   75   80

Ala Val Gly Ala Ile Val Leu Thr Gly Gly Asp Lys Ala Phe Ala Ala
                    85   90   95

Gly Ala Asp Ile Lys Glu Met Gln Asn Leu Ser Phe Gln Asp Cys Tyr
10   100   105   110

Ser Ser Lys Phe Leu Lys His Trp Asp His Leu Thr Gln Val Lys Lys
                    115   120   125

Pro Val Ile Ala Ala Val Asn Gly Tyr Ala Phe Gly Gly Gly Cys Glu
                    130   135   140

15 Leu Ala Met Met Cys Asp Ile Ile Tyr Ala Gly Glu Lys Ala Gln Phe
                145   150   155   160

Ala Gln Pro Glu Ile Leu Ile Gly Thr Ile Pro Gly Ala Gly Gly Thr
                    165   170   175

Gln Arg Leu Thr Arg Ala Val Gly Lys Ser Leu Ala Met Glu Met Val
20   180   185   190

Leu Thr Gly Asp Arg Ile Ser Ala Gln Asp Ala Lys Gln Ala Gly Leu
                195   200   205

Val Ser Lys Ile Cys Pro Val Glu Thr Leu Val Glu Glu Ala Ile Gln
                210   215   220

Cys Ala Glu Lys Ile Ala Ser Asn Ser Lys Ile Val Val Ala Met Ala

    225   230   235   240

Lys Glu Ser Val Asn Ala Ala Phe Glu Met Thr Leu Thr Glu Gly Ser

              245   250   255

5   Lys Leu Glu Lys Lys Leu Phe Tyr Ser Thr Phe Ala Thr Asp Asp Arg

              260   265   270

Lys Glu Gly Met Thr Ala Phe Val Glu Lys Arg Lys Ala Asn Phe Lys

          275   280   285

Asp Gln

10   290

<210> 38

<211> 160

15 <212> PRT

<213> Homo sapiens

<220>

<221> Heat-shock 20 kDa like-protein p20

<222> (1)..(160)

20 <223> Accession No. as of 09 Dec 2002: O14558

<400> 38

Met Glu Ile Pro Val Pro Val Gln Pro Ser Trp Leu Arg Arg Ala Ser

    1   5   10   15

Ala Pro Leu Pro Gly Leu Ser Ala Pro Gly Arg Leu Phe Asp Gln Arg
                20   25   30

Phe Gly Glu Gly Leu Leu Glu Ala Glu Leu Ala Ala Leu Cys Pro Thr
                35   40   45

5   Thr Leu Ala Pro Tyr Tyr Leu Arg Ala Pro Ser Val Ala Leu Pro Val
                50   55   60

Ala Gln Val Pro Thr Asp Pro Gly His Phe Ser Val Leu Leu Asp Val
65   70   75   80

Lys His Phe Ser Pro Glu Glu Ile Ala Val Lys Val Val Gly Glu His
10   85   90   95

Val Glu Val His Ala Arg His Glu Glu Arg Pro Asp Glu His Gly Phe
                100   105   110

Val Ala Arg Glu Phe His Arg Arg Tyr Arg Leu Pro Pro Gly Val Asp
                115   120   125

15   Pro Ala Ala Val Thr Ser Ala Leu Ser Pro Glu Gly Val Leu Ser Ile
                130   135   140

Gln Ala Ala Pro Ala Ser Ala Gln Ala Pro Pro Pro Ala Ala Ala Lys
145   150   155   160

20

<210>   39

<211>   151

<212>   PRT

<213>   Homo sapiens

<220>

<221> Myosin light chain alkali, non-muscle isoform

<222> (1)..(151)

<223> Accession No. as of 09 Dec 2002: P16475

5   <400> 39

    Met Cys Asp Phe Thr Glu Asp Gln Thr Ala Glu Phe Lys Glu Ala Phe

    1   5   10   15

    Gln Leu Phe Asp Arg Thr Gly Asp Gly Lys Ile Leu Tyr Ser Gln Cys

10   20   25   30

    Gly Asp Val Met Arg Ala Leu Gly Gln Asn Pro Thr Asn Ala Glu Val

                    35   40   45

    Leu Lys Val Leu Gly Asn Pro Lys Ser Asp Glu Met Asn Val Lys Val

                    50   55   60

15 Leu Asp Phe Glu His Phe Leu Pro Met Leu Gln Thr Val Ala Lys Asn

    65   70   .   75   80

    Lys Asp Gln Gly Thr Tyr Glu Asp Tyr Val Glu Gly Leu Arg Val Phe

                        85   90   95

    Asp Lys Glu Gly Asn Gly Thr Val Met Gly Ala Glu Ile Arg His Val

20   100   105   110

    Leu Val Thr Leu Gly Glu Lys Met Thr Glu Glu Glu Val Glu Met Leu

                    115   120   125

    Val Ala Gly His Glu Asp Ser Asn Gly Cys Ile Asn Tyr Glu Ala Phe

                    130   135   140

Val Arg His Ile Leu Ser Gly

145   150

5   <210>   40

     <211>   592

     <212>   PRT

     <213>   Homo sapiens

     <220>

10   <221>   Calnexin precursor

     <222>   (1)..(592)

     <223>   Accession No. as of 09 Dec 2002: P27824

     <400>   40

15   Met Glu Gly Lys Trp Leu Leu Cys Met Leu Leu Val Leu Gly Thr Ala

     1   5   10   15

     Ile Val Glu Ala His Asp Gly His Asp Asp Val Ile Asp Ile Glu

                 20   25   30

     Asp Asp Leu Asp Asp Val Ile Glu Glu Val Glu Asp Ser Lys Pro Asp

20   35   40   45

     Thr Thr Ala Pro Pro Ser Ser Pro Lys Val Thr Tyr Lys Ala Pro Val

             50   55   60

     Pro Thr Gly Glu Val Tyr Phe Ala Asp Ser Phe Asp Arg Gly Thr Leu

     65   70   75   80

```
   Ser Gly Trp Ile Leu Ser Lys Ala Lys Lys Asp Asp Thr Asp Asp Glu
                       85                90                95

   Ile Ala Lys Tyr Asp Gly Lys Trp Glu Val Glu Glu Met Lys Glu Ser
                      100               105               110

 5 Lys Leu Pro Gly Asp Lys Gly Leu Val Leu Met Ser Arg Ala Lys His
                      115               120               125

   His Ala Ile Ser Ala Lys Leu Asn Lys Pro Phe Leu Phe Asp Thr Lys
                      130               135               140

   Pro Leu Ile Val Gln Tyr Glu Val Asn Phe Gln Asn Gly Ile Glu Cys
10 145                  150               155                   160

   Gly Gly Ala Tyr Val Lys Leu Leu Ser Lys Thr Pro Glu Leu Asn Leu
                      165               170               175

   Asp Gln Phe His Asp Lys Thr Pro Tyr Thr Ile Met Phe Gly Pro Asp
                      180               185               190

15 Lys Cys Gly Glu Asp Tyr Lys Leu His Phe Ile Phe Arg His Lys Asn
                      195               200               205

   Pro Lys Thr Gly Ile Tyr Glu Glu Lys His Ala Lys Arg Pro Asp Ala
                      210               215               220

   Asp Leu Lys Thr Tyr Phe Thr Asp Lys Lys Thr His Leu Tyr Thr Leu
20 225                  230               235                   240

   Ile Leu Asn Pro Asp Asn Ser Phe Glu Ile Leu Val Asp Gln Ser Val
                      245               250               255

   Val Asn Ser Gly Asn Leu Leu Asn Asp Met Thr Pro Pro Val Asn Pro
                      260               265               270
```

Ser Arg Glu Ile Glu Asp Pro Glu Asp Arg Lys Pro Glu Asp Trp Asp

         275   280   285

Glu Arg Pro Lys Ile Pro Asp Pro Glu Ala Val Lys Pro Asp Asp Trp

         290   295   300

5   Asp Glu Asp Ala Pro Ala Lys Ile Pro Asp Glu Glu Ala Thr Lys Pro

     305   310   315   320

Glu Gly Trp Leu Asp Asp Glu Pro Glu Tyr Val Pro Asp Pro Asp Ala

              325   330   335

Glu Lys Pro Glu Asp Trp Asp Glu Asp Met Asp Gly Glu Trp Glu Ala

10   340   345   350

Pro Gln Ile Ala Asn Pro Arg Cys Glu Ser Ala Pro Gly Cys Gly Val

              355   360   365

Trp Gln Arg Pro Val Ile Asp Asn Pro Asn Tyr Lys Gly Lys Trp Lys

              370   375   380

15   Pro Pro Met Ile Asp Asn Pro Ser Tyr Gln Gly Ile Trp Lys Pro Arg

     385   390   395   400

Lys Ile Pro Asn Pro Asp Phe Phe Glu Asp Leu Glu Pro Phe Arg Met

              405   410   415

Thr Pro Phe Ser Ala Ile Gly Leu Glu Leu Trp Ser Met Thr Ser Asp

20   420   425   430

Ile Phe Phe Asp Asn Phe Ile Ile Cys Ala Asp Arg Arg Ile Val Asp

              435   440   445

Asp Trp Ala Asn Asp Gly Trp Gly Leu Lys Lys Ala Ala Asp Gly Ala

              450   455   460

Ala Glu Pro Gly Val Val Gly Gln Met Ile Glu Ala Ala Glu Glu Arg

465   470   475   480

Pro Trp Leu Trp Val Val Tyr Ile Leu Thr Val Ala Leu Pro Val Phe

                485   490   495

5   Leu Val Ile Leu Phe Cys Cys Ser Gly Lys Lys Gln Thr Ser Gly Met

                500   505   510

Glu Tyr Lys Lys Thr Asp Ala Pro Gln Pro Asp Val Lys Glu Glu Glu

            515   520   525

Glu Glu Lys Glu Glu Glu Lys Asp Lys Gly Asp Glu Glu Glu Glu Gly

10   530   535   540

Glu Glu Lys Leu Glu Glu Lys Gln Lys Ser Asp Ala Glu Glu Asp Gly

545   550   555   560

Gly Thr Val Ser Gln Glu Glu Glu Asp Arg Lys Pro Lys Ala Glu Glu

                565   570   575

15 Asp Glu Ile Leu Asn Arg Ser Pro Arg Asn Arg Lys Pro Arg Arg Glu

            580   585   590

<210>   41

20 <211>   282

<212>   PRT

<213>   Homo sapiens

<220>

<221>   Complement component 1

<222>   (1)..(282)

<223>   Accession No. as of 09 Dec 2002: Q07021

<400>   41

5   Met Leu Pro Leu Leu Arg Cys Val Pro Arg Val Leu Gly Ser Ser Val
     1   5   10   15

     Ala Gly Leu Arg Ala Ala Ala Pro Ala Ser Pro Phe Arg Gln Leu Leu
                 20   25   30

     Gln Pro Ala Pro Arg Leu Cys Thr Arg Pro Phe Gly Leu Leu Ser Val
10   35   40   45

     Arg Ala Gly Ser Glu Arg Arg Pro Gly Leu Leu Arg Pro Arg Gly Pro
                 50   55   60

     Cys Ala Cys Gly Cys Gly Cys Gly Ser Leu His Thr Asp Gly Asp Lys
     65   70   75   80

15   Ala Phe Val Asp Phe Leu Ser Asp Glu Ile Lys Glu Glu Arg Lys Ile
                     85   90   95

     Gln Lys His Lys Thr Leu Pro Lys Met Ser Gly Gly Trp Glu Leu Glu
                 100   105   110

     Leu Asn Gly Thr Glu Ala Lys Leu Val Arg Lys Val Ala Gly Glu Lys
20   115   120   125

     Ile Thr Val Thr Phe Asn Ile Asn Asn Ser Ile Pro Pro Thr Phe Asp
                 130   135   140

     Gly Glu Glu Glu Pro Ser Gln Gly Gln Lys Val Glu Glu Gln Glu Pro
     145   150   155   160

Glu Leu Thr Ser Thr Pro Asn Phe Val Val Glu Val Ile Lys Asn Asp
                165   170   175

Asp Gly Lys Lys Ala Leu Val Leu Asp Cys His Tyr Pro Glu Asp Glu
                180   185   190

5   Val Gly Gln Glu Asp Glu Ala Glu Ser Asp Ile Phe Ser Ile Arg Glu
                195   200   205

Val Ser Phe Gln Ser Thr Gly Glu Ser Glu Trp Lys Asp Thr Asn Tyr
                210   215   220

Thr Leu Asn Thr Asp Ser Leu Asp Trp Ala Leu Tyr Asp His Leu Met
10 225   230   235   240

Asp Phe Leu Ala Asp Arg Gly Val Asp Asn Thr Phe Ala Asp Glu Leu
                245   250   255

Val Glu Leu Ser Thr Ala Leu Glu His Gln Glu Tyr Ile Thr Phe Leu
                260   265   270

15 Glu Asp Leu Lys Ser Phe Val Lys Ser Gln
                275   280

<210> 42

20 <211> 727

<212> PRT

<213> Homo sapiens

<220>

<221> NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial

precursor

<222>   (1)..(727)

<223>   Accession No. as of 09 Dec 2002: P28331

<400>   42

5

Met Leu Arg Ile Pro Val Arg Arg Ala Leu Val Gly Leu Ser Lys Ser
1   5   10   15

Pro Lys Gly Cys Val Arg Thr Thr Ala Thr Ala Ala Ser Asn Leu Ile
                20   25   30

10 Glu Val Phe Val Asp Gly Gln Ser Val Met Val Glu Pro Gly Thr Thr
                35   40   45

Val Leu Gln Ala Cys Glu Lys Val Gly Met Gln Ile Pro Arg Phe Cys
            50   55   60

Tyr His Glu Arg Leu Ser Val Ala Gly Asn Cys Arg Met Cys Leu Val
15 65   70   75   80

Glu Ile Glu Lys Ala Pro Lys Val Val Ala Ala Cys Ala Met Pro Val
                85   90   95

Met Lys Gly Trp Asn Ile Leu Thr Asn Ser Glu Lys Ser Lys Lys Ala
                100   105   110

20 Arg Glu Gly Val Met Glu Phe Leu Leu Ala Asn His Pro Leu Asp Cys
                115   120   125

Pro Ile Cys Asp Gln Gly Gly Glu Cys Asp Leu Gln Asp Gln Ser Met
            130   135   140

Met Phe Gly Asn Asp Arg Ser Arg Phe Leu Glu Gly Lys Arg Ala Val

```
                145                    150                    155                    160

      Glu Asp Lys Asn Ile Gly Pro Leu Val Lys Thr Ile Met Thr Arg Cys

                        165                    170                    175

      Ile Gln Cys Thr Arg Cys Ile Arg Phe Ala Ser Glu Ile Ala Gly Val

 5                      180                    185                    190

      Asp Asp Leu Gly Thr Thr Gly Arg Gly Asn Asp Met Gln Val Gly Thr

                195                    200                    205

      Tyr Ile Glu Lys Met Phe Met Ser Glu Leu Ser Gly Asn Ile Ile Asp

                210                    215                    220

10    Ile Cys Pro Val Gly Ala Leu Thr Ser Lys Pro Tyr Ala Phe Thr Ala

      225                    230                    235                    240

      Arg Pro Trp Glu Thr Arg Lys Thr Glu Ser Ile Asp Val Met Asp Ala

                        245                    250                    255

      Val Gly Ser Asn Ile Val Val Ser Thr Arg Thr Gly Glu Val Met Arg

15                      260                    265                    270

      Ile Leu Pro Arg Met His Glu Asp Ile Asn Glu Glu Trp Ile Ser Asp

                275                    280                    285

      Lys Thr Arg Phe Ala Tyr Asp Gly Leu Lys Arg Gln Arg Leu Thr Glu

                290                    295                    300

20    Pro Met Val Arg Asn Glu Lys Gly Leu Leu Thr Tyr Thr Ser Trp Glu

      305                    310                    315                    320

      Asp Ala Leu Ser Arg Val Ala Gly Met Leu Gln Ser Phe Gln Gly Lys

                325                    330                    335

      Asp Val Ala Ala Ile Ala Gly Gly Leu Val Asp Ala Glu Ala Leu Val
```

                      340   345   350

      Ala Leu Lys Asp Leu Leu Asn Arg Val Asp Ser Asp Thr Leu Cys Thr

                355   360   365

      Glu Glu Val Phe Pro Thr Ala Gly Ala Gly Thr Asp Leu Arg Ser Asn

    5   370   375   380

      Tyr Leu Leu Asn Thr Thr Ile Ala Gly Val Glu Glu Ala Asp Val Val

      385   390   395   400

      Leu Leu Val Gly Thr Asn Pro Arg Phe Glu Ala Pro Leu Phe Asn Ala

                          405   410   415

   10 Trp Ile Arg Lys Ser Trp Leu His Asn Asp Leu Lys Val Ala Leu Ile

                420   425   430

      Gly Ser Pro Val Asp Leu Thr Tyr Thr Tyr Asp His Leu Gly Asp Ser

                435   440   445

      Pro Lys Ile Leu Gln Asp Ile Ala Ser Gly Ser His Pro Phe Ser Gln

   15   450   455   460

      Val Leu Lys Glu Ala Lys Lys Pro Met Val Val Leu Gly Ser Ser Ala

      465   470   475   480

      Leu Gln Arg Asn Asp Gly Ala Ala Ile Leu Ala Ala Val Ser Ser Ile

                          485   490   495

   20 Ala Gln Lys Ile Arg Met Thr Ser Gly Val Thr Gly Asp Trp Lys Val

                500   505   510

      Met Asn Ile Leu His Arg Ile Ala Ser Gln Val Ala Ala Leu Asp Leu

                515   520   525

      Gly Tyr Lys Pro Gly Val Glu Ala Ile Arg Lys Asn Pro Pro Lys Val

```
                530                    535                    540

      Leu Phe Leu Leu Gly Ala Asp Gly Gly Cys Ile Thr Arg Gln Asp Leu

            545                    550                    555                    560

      Pro Lys Asp Cys Phe Ile Ile Tyr Gln Gly His His Gly Asp Val Gly

  5                        565                    570                    575

      Ala Pro Ile Ala Asp Val Ile Leu Pro Gly Ala Ala Tyr Thr Glu Lys

                        580                    585                    590

      Ser Ala Thr Tyr Val Asn Thr Glu Gly Arg Ala Gln Gln Thr Lys Val

                    595                    600                    605

 10   Ala Val Thr Pro Pro Gly Leu Ala Arg Glu Asp Trp Lys Ile Ile Arg

              610                    615                    620

      Ala Leu Ser Glu Ile Ala Gly Met Thr Leu Pro Tyr Asp Thr Leu Asp

      625                    630                    635                    640

      Gln Val Arg Asn Arg Leu Glu Glu Phe Ser Pro Asn Leu Val Arg Tyr

 15                        645                    650                    655

      Asp Asp Ile Glu Gly Ala Asn Tyr Phe Gln Gln Ala Asn Glu Leu Ser

                    660                    665                    670

      Lys Leu Val Asn Gln Gln Leu Leu Ala Asp Pro Leu Val Pro Pro Gln

                675                    680                    685

 20   Leu Thr Leu Lys Asp Phe Tyr Met Thr Asp Ser Ile Ser Arg Ala Ser

            690                    695                    700

      Gln Thr Met Ala Lys Cys Val Lys Ala Val Thr Glu Gly Ala Gln Ala

      705                    710                    715                    720

      Val Glu Glu Pro Ser Ile Cys
```

725

        <210>   43

    5   <211>   491

        <212>   PRT

        <213>   Homo sapiens

        <220>

        <221>   Pre-B cell enhancing factor precursor

    10 <222>   (1)..(491)

        <223>   Accession No. as of 09 Dec 2002: P43490

        <400>   43

        Met Asn Pro Ala Ala Glu Ala Glu Phe Asn Ile Leu Leu Ala Thr Asp
    15 1   5   10   15

        Ser Tyr Lys Val Thr His Tyr Lys Gln Tyr Pro Pro Asn Thr Ser Lys
                        20   25   30

        Val Tyr Ser Tyr Phe Glu Cys Arg Glu Lys Lys Thr Glu Asn Ser Lys
                        35   40   45

    20 Leu Arg Lys Val Lys Tyr Glu Glu Thr Val Phe Tyr Gly Leu Gln Tyr
                50   55   60

        Ile Leu Asn Lys Tyr Leu Lys Gly Lys Val Val Thr Lys Glu Lys Ile
        65   70   75   80

        Gln Glu Ala Lys Asp Val Tyr Lys Glu His Phe Gln Asp Asp Val Phe

                              85   90   95

        Asn Glu Lys Gly Trp Asn Tyr Ile Leu Glu Lys Tyr Asp Gly His Leu

                        100   105   110

        Pro Ile Glu Ile Lys Ala Val Pro Glu Gly Phe Val Ile Pro Arg Gly

  5   115   120   125

        Asn Val Leu Phe Thr Val Glu Asn Thr Asp Pro Glu Cys Tyr Trp Leu

                  130   135   140

        Thr Asn Trp Ile Glu Thr Ile Leu Val Gln Ser Trp Tyr Pro Ile Thr

        145   150   155   160

  10   Val Ala Thr Asn Ser Arg Glu Gln Lys Lys Ile Leu Ala Lys Tyr Leu

                        165   170   175

        Leu Glu Thr Ser Gly Asn Leu Asp Gly Leu Glu Tyr Lys Leu His Asp

                        180   185   190

        Phe Gly Tyr Arg Gly Val Ser Ser Gln Glu Thr Ala Gly Ile Gly Ala

  15   195   200   205

        Ser Ala His Leu Val Asn Phe Lys Gly Thr Asp Thr Val Ala Gly Leu

                  210   215   220

        Ala Leu Ile Lys Lys Tyr Tyr Gly Thr Lys Asp Pro Val Pro Gly Tyr

        225   230   235   240

  20   Ser Val Pro Ala Ala Glu His Ser Thr Ile Thr Ala Trp Gly Lys Asp

                  245   250   255

        His Glu Lys Asp Ala Phe Glu His Ile Val Thr Gln Phe Ser Ser Val

                  260   265   270

        Pro Val Ser Val Val Ser Asp Ser Tyr Asp Ile Tyr Asn Ala Cys Glu

```
                   275                 280                 285
       Lys Ile Trp Gly Glu Asp Leu Arg His Leu Ile Val Ser Arg Ser Thr
                   290                 295                 300
       Gln Ala Pro Leu Ile Ile Arg Pro Asp Ser Gly Asn Pro Leu Asp Thr
   5   305                 310                 315                 320
       Val Leu Lys Val Leu Glu Ile Leu Gly Lys Lys Phe Pro Val Thr Glu
                           325                 330                 335
       Asn Ser Lys Gly Tyr Lys Leu Leu Pro Pro Tyr Leu Arg Val Ile Gln
                           340                 345                 350
  10   Gly Asp Gly Val Asp Ile Asn Thr Leu Gln Glu Ile Val Glu Gly Met
                   355                 360                 365
       Lys Gln Lys Met Trp Ser Ile Glu Asn Ile Ala Phe Gly Ser Gly Gly
                   370                 375                 380
       Gly Leu Leu Gln Lys Leu Thr Arg Asp Leu Leu Asn Cys Ser Phe Lys
  15   385                 390                 395                 400
       Cys Ser Tyr Val Val Thr Asn Gly Leu Gly Ile Asn Val Phe Lys Asp
                           405                 410                 415
       Pro Val Ala Asp Pro Asn Lys Arg Ser Lys Lys Gly Arg Leu Ser Leu
                           420                 425                 430
  20   His Arg Thr Pro Ala Gly Asn Phe Val Thr Leu Glu Glu Gly Lys Gly
                   435                 440                 445
       Asp Leu Glu Glu Tyr Gly Gln Asp Leu Leu His Thr Val Phe Lys Asn
                   450                 455                 460
       Gly Lys Val Thr Lys Ser Tyr Ser Phe Asp Glu Ile Arg Lys Asn Ala
```

                465   470   475   480

        Gln Leu Asn Ile Glu Leu Glu Ala Ala His His

                        485   490

    5

        <210> 44

        <211> 135

        <212> PRT

        <213> Homo sapiens

10 <220>

        <221> Retinol-binding protein I, cellular

        <222> (1)..(135)

        <223> Accession No. as of 09 Dec 2002: P09455

        <400> 44

15

    Met Pro Val Asp Phe Thr Gly Tyr Trp Lys Met Leu Val Asn Glu Asn

    1   5   10   15

    Phe Glu Glu Tyr Leu Arg Ala Leu Asp Val Asn Val Ala Leu Arg Lys

                    20   25   30

20 Ile Ala Asn Leu Leu Lys Pro Asp Lys Glu Ile Val Gln Asp Gly Asp

                    35   40   45

    His Met Ile Ile Arg Thr Leu Ser Thr Phe Arg Asn Tyr Ile Met Asp

            50   55   60

    Phe Gln Val Gly Lys Glu Phe Glu Glu Asp Leu Thr Gly Ile Asp Asp

```
     65                    70                   75                   80

   Arg Lys Cys Met Thr Thr Val Ser Trp Asp Gly Asp Lys Leu Gln Cys

                      85                   90                   95

   Val Gln Lys Gly Glu Lys Glu Gly Arg Gly Trp Thr Gln Trp Ile Glu

5                    100                  105                  110

   Gly Asp Glu Leu His Leu Glu Met Arg Val Glu Gly Val Val Cys Lys

                     115                  120                  125

   Gln Val Phe Lys Lys Val Gln

               130                  135

10
```

<210>   45

<211>   544

<212>   PRT

<213>   Homo sapiens

<220>

<221>   T-complex protein 1, gamma subunit

<222>   (1)..(544)

<223>   Accession No. as of 09 Dec 2002: P49368

<400>   45

```
   Met Gly His Arg Pro Val Leu Val Leu Ser Gln Asn Thr Lys Arg Glu

   1                5                   10                   15

   Ser Gly Arg Lys Val Gln Ser Gly Asn Ile Asn Ala Ala Lys Thr Ile
```

                    20   25   30

        Ala Asp Ile Ile Arg Thr Cys Leu Gly Pro Lys Ser Met Met Lys Met

                    35   40   45

        Leu Leu Asp Pro Met Gly Gly Ile Val Met Thr Asn Asp Gly Asn Ala

    5   50   55   60

        Ile Leu Arg Glu Ile Gln Val Gln His Pro Ala Ala Lys Ser Met Ile

        65   70   75   80

        Glu Ile Ser Arg Thr Gln Asp Glu Glu Val Gly Asp Gly Thr Thr Ser

                         85   90   95

    10 Val Ile Ile Leu Ala Gly Glu Met Leu Ser Val Ala Glu His Phe Leu

                    100   105   110

        Glu Gln Gln Met His Pro Thr Val Val Ile Ser Ala Tyr Arg Lys Ala

                    115   120   125

        Leu Asp Asp Met Ile Ser Thr Leu Lys Lys Ile Ser Ile Pro Val Asp

    15   130   135   140

        Ile Ser Asp Ser Asp Met Met Leu Asn Ile Ile Asn Ser Ser Ile Thr

        145   150   155   160

        Thr Lys Ala Ile Ser Arg Trp Ser Ser Leu Ala Cys Asn Ile Ala Leu

                    165   170   175

    20 Asp Ala Val Lys Met Val Gln Phe Glu Glu Asn Gly Arg Lys Glu Ile

                    180   185   190

        Asp Ile Lys Lys Tyr Ala Arg Val Glu Lys Ile Pro Gly Gly Ile Ile

                    195   200   205

        Glu Asp Ser Cys Val Leu Arg Gly Val Met Ile Asn Lys Asp Val Thr

```
         210                    215                       220

   His Pro Arg Met Arg Arg Tyr Ile Lys Asn Pro Arg Ile Val Leu Leu

         225                    230          235                  240

   Asp Ser Ser Leu Glu Tyr Lys Lys Gly Glu Ser Gln Thr Asp Ile Glu

5                    245              250                   255

   Ile Thr Arg Glu Glu Asp Phe Thr Arg Ile Leu Gln Met Glu Glu Glu

               260              265                270

   Tyr Ile Gln Gln Leu Cys Glu Asp Ile Ile Gln Leu Lys Pro Asp Val

            275              280                285

10  Val Ile Thr Glu Lys Gly Ile Ser Asp Leu Ala Gln His Tyr Leu Met

            290              295                300

   Arg Ala Asn Ile Thr Ala Ile Arg Arg Val Arg Lys Thr Asp Asn Asn

   305                310                315                  320

   Arg Ile Ala Arg Ala Cys Gly Ala Arg Ile Val Ser Arg Pro Glu Glu

15                   325              330                   335

   Leu Arg Glu Asp Asp Val Gly Thr Gly Ala Gly Leu Leu Glu Ile Lys

               340              345                350

   Lys Ile Gly Asp Glu Tyr Phe Thr Phe Ile Thr Asp Cys Lys Asp Pro

            355              360                365

20  Lys Ala Cys Thr Ile Leu Leu Arg Gly Ala Ser Lys Glu Ile Leu Ser

            370              375                380

   Glu Val Glu Arg Asn Leu Gln Asp Ala Met Gln Val Cys Arg Asn Val

   385                390                395                  400

   Leu Leu Asp Pro Gln Leu Val Pro Gly Gly Gly Ala Ser Glu Met Ala
```

```
                    405                    410                    415

     Val Ala His Ala Leu Thr Glu Lys Ser Lys Ala Met Thr Gly Val Glu

               420                    425                    430

     Gln Trp Pro Tyr Arg Ala Val Ala Gln Ala Leu Glu Val Ile Pro Arg

5              435                    440                    445

     Thr Leu Ile Gln Asn Cys Gly Ala Ser Thr Ile Arg Leu Leu Thr Ser

          450                    455                    460

     Leu Arg Ala Lys His Thr Gln Glu Asn Cys Glu Thr Trp Gly Val Asn

     465                    470                    475                    480

10   Gly Glu Thr Gly Thr Leu Val Asp Met Lys Glu Leu Gly Ile Trp Glu

                    485                    490                    495

     Pro Leu Ala Val Lys Leu Gln Thr Tyr Lys Thr Ala Val Glu Thr Ala

               500                    505                    510

     Val Leu Leu Leu Arg Ile Asp Asp Ile Val Ser Gly His Lys Lys Lys

15             515                    520                    525

     Gly Asp Asp Gln Ser Arg Gln Gly Gly Ala Pro Asp Ala Gly Gln Glu

          530                    535                    540
```

20   <210>   46

     <211>   461

     <212>   PRT

     <213>   Homo sapiens

     <220>

<221>   Placental ribonuclease inhibitor

<222>   (1)..(461)

<223>   Accession No. as of 09 Dec 2002: P13489

<400>   46

5

Met Ser Leu Asp Ile Gln Ser Leu Asp Ile Gln Cys Glu Glu Leu Ser

1   5   10   15

Asp Ala Arg Trp Ala Glu Leu Leu Pro Leu Leu Gln Gln Cys Gln Val

                20   25   30

10 Val Arg Leu Asp Asp Cys Gly Leu Thr Glu Ala Arg Cys Lys Asp Ile

                35   40   45

Ser Ser Ala Leu Arg Val Asn Pro Ala Leu Ala Glu Leu Asn Leu Arg

        50   55   60

Ser Asn Glu Leu Gly Asp Val Gly Val His Cys Val Leu Gln Gly Leu

15 65   70   75   80

Gln Thr Pro Ser Cys Lys Ile Gln Lys Leu Ser Leu Gln Asn Cys Cys

                85   90   95

Leu Thr Gly Ala Gly Cys Gly Val Leu Ser Ser Thr Leu Arg Thr Leu

                100   105   110

20 Pro Thr Leu Gln Glu Leu His Leu Ser Asp Asn Leu Leu Gly Asp Ala

                115   120   125

Gly Leu Gln Leu Leu Cys Glu Gly Leu Leu Asp Pro Gln Cys Arg Leu

        130   135   140

Glu Lys Leu Gln Leu Glu Tyr Cys Ser Leu Ser Ala Ala Ser Cys Glu

```
        145                 150                 155                 160
      Pro Leu Ala Ser Val Leu Arg Ala Lys Pro Asp Phe Lys Glu Leu Thr

                 165                 170                 175
      Val Ser Asn Asn Asp Ile Asn Glu Ala Gly Val Arg Val Leu Cys Gln

   5             180                 185                 190
      Gly Leu Lys Asp Ser Pro Cys Gln Leu Glu Ala Leu Lys Leu Glu Ser

            195                 200                 205
      Cys Gly Val Thr Ser Asp Asn Cys Arg Asp Leu Cys Gly Ile Val Ala

            210                 215                 220
  10  Ser Lys Ala Ser Leu Arg Glu Leu Ala Leu Gly Ser Asn Lys Leu Gly

      225                 230                 235                 240
      Asp Val Gly Met Ala Glu Leu Cys Pro Gly Leu Leu His Pro Ser Ser

                 245                 250                 255
      Arg Leu Arg Thr Leu Trp Ile Trp Glu Cys Gly Ile Thr Ala Lys Gly

  15            260                 265                 270
      Cys Gly Asp Leu Cys Arg Val Leu Arg Ala Lys Glu Ser Leu Lys Glu

            275                 280                 285
      Leu Ser Leu Ala Gly Asn Glu Leu Gly Asp Glu Gly Ala Arg Leu Leu

            290                 295                 300
  20  Cys Glu Thr Leu Leu Glu Pro Gly Cys Gln Leu Glu Ser Leu Trp Val

      305                 310                 315                 320
      Lys Ser Cys Ser Phe Thr Ala Ala Cys Cys Ser His Phe Ser Ser Val

                 325                 330                 335
      Leu Ala Gln Asn Arg Phe Leu Leu Glu Leu Gln Ile Ser Asn Asn Arg
```

                    340   345   350

        Leu Glu Asp Ala Gly Val Arg Glu Leu Cys Gln Gly Leu Gly Gln Pro

                    355   360   365

        Gly Ser Val Leu Arg Val Leu Trp Leu Ala Asp Cys Asp Val Ser Asp

   5   370   375   380

        Ser Ser Cys Ser Ser Leu Ala Ala Thr Leu Leu Ala Asn His Ser Leu

        385   390   395   400

        Arg Glu Leu Asp Leu Ser Asn Asn Cys Leu Gly Asp Ala Gly Ile Leu

                        405   410   415

   10   Gln Leu Val Glu Ser Val Arg Gln Pro Gly Cys Leu Leu Glu Gln Leu

                    420   425   430

        Val Leu Tyr Asp Ile Tyr Trp Ser Glu Glu Met Glu Asp Arg Leu Gln

                    435   440   445

        Ala Leu Glu Lys Asp Lys Pro Ser Leu Arg Val Ile Ser

   15   450   455   460

        <210>   47

        <211>   317

   20   <212>   PRT

        <213>   Homo sapiens

        <220>

        <221>   Guanine nucleotide-binding protein beta subunit-like protein
        12.3

<222>   (1)..(317)

<223>   Accession No. as of 09 Dec 2002: P25388

<400>   47

Met Thr Glu Gln Met Thr Leu Arg Gly Thr Leu Lys Gly His Asn Gly
 1   5   10   15

Trp Val Thr Gln Ile Ala Thr Thr Pro Gln Phe Pro Asp Met Ile Leu
            20   25   30

Ser Ala Ser Arg Asp Lys Thr Ile Ile Met Trp Lys Leu Thr Arg Asp
        35   40   45

Glu Thr Asn Tyr Gly Ile Pro Gln Arg Ala Leu Arg Gly His Ser His
        50   55   60

Phe Val Ser Asp Val Val Ile Ser Ser Asp Gly Gln Phe Ala Leu Ser
65   70   75   80

Gly Ser Trp Asp Gly Thr Leu Arg Leu Trp Asp Leu Thr Thr Gly Thr
                85   90   95

Thr Thr Arg Arg Phe Val Gly His Thr Lys Asp Val Leu Ser Val Ala
            100   105   110

Phe Ser Ser Asp Asn Arg Gln Ile Val Ser Gly Ser Arg Asp Lys Thr
        115   120   125

Ile Lys Leu Trp Asn Thr Leu Gly Val Cys Lys Tyr Thr Val Gln Asp
        130   135   140

Glu Ser His Ser Glu Trp Val Ser Cys Val Arg Phe Ser Pro Asn Ser
145   150   155   160

Ser Asn Pro Ile Ile Val Ser Cys Gly Trp Asp Lys Leu Val Lys Val

                    165   170   175

Trp Asn Leu Ala Asn Cys Lys Leu Lys Thr Asn His Ile Gly His Thr

                    180   185   190

5   Gly Tyr Leu Asn Thr Val Thr Val Ser Pro Asp Gly Ser Leu Cys Ala

                195   200   205

    Ser Gly Gly Lys Asp Gly Gln Ala Met Leu Trp Asp Leu Asn Glu Gly

            210   215   220

    Lys His Leu Tyr Thr Leu Asp Gly Gly Asp Ile Ile Asn Ala Leu Cys

10 225   230   235   240

    Phe Ser Pro Asn Arg Tyr Trp Leu Cys Ala Ala Thr Gly Pro Ser Ile

                245   250   255

    Lys Ile Trp Asp Leu Glu Gly Lys Ile Ile Val Asp Glu Leu Lys Gln

                260   265   270

15 Glu Val Ile Ser Thr Ser Ser Lys Ala Glu Pro Pro Gln Cys Thr Ser

                275   280   285

    Leu Ala Trp Ser Ala Asp Gly Gln Thr Leu Phe Ala Gly Tyr Thr Asp

                290   295   300

    Asn Leu Val Arg Val Trp Gln Val Thr Ile Gly Thr Arg

20 305   310   315

    <210> 48

    <211> 172

<212> PRT

<213> Homo sapiens

<220>

<221> Myosin regulatory light chain 2

5   <222> (1)..(172)

<223> Accession No. as of 10 Dec 2002: P24844

<400> 48

Met Ser Ser Lys Arg Ala Lys Ala Lys Thr Thr Lys Lys Arg Pro Gln

10 1   5   10   15

Arg Ala Thr Ser Asn Val Phe Ala Met Phe Asp Gln Ser Gln Ile Gln

                20   25   30

Glu Phe Lys Glu Ala Phe Asn Met Ile Asp Gln Asn Arg Asp Gly Phe

                35   40   45

15 Ile Asp Lys Glu Asp Leu His Asp Met Leu Ala Ser Leu Gly Lys Asn

            50   55   60

Pro Thr Asp Glu Tyr Leu Glu Gly Met Met Ser Glu Ala Pro Gly Pro

65   70   75   80

Ile Asn Phe Thr Met Phe Leu Thr Met Phe Gly Glu Lys Leu Asn Gly

20   85   90   95

Thr Asp Pro Glu Asp Val Ile Arg Asn Ala Phe Ala Cys Phe Asp Glu

                100   105   110

Glu Ala Ser Gly Phe Ile His Glu Asp His Leu Arg Glu Leu Leu Thr

            115   120   125

```
     Thr Met Gly Asp Arg Phe Thr Asp Glu Glu Val Asp Glu Met Tyr Arg

         130                 135                 140

     Glu Ala Pro Ile Asp Lys Lys Gly Asn Phe Asn Tyr Val Glu Phe Thr

     145                 150                 155                 160

  5  Arg Ile Leu Lys His Gly Ala Lys Asp Lys Asp Asp

             165                 170
```

```
     <210>  49

 10  <211>  114

     <212>  PRT

     <213>  Homo sapiens

     <220>

     <221>  Calgranulin B

 15  <222>  (1)..(114)

     <223>  Accession No. as of 10 Dec 2002: P06702

     <400>  49


     Met Thr Cys Lys Met Ser Gln Leu Glu Arg Asn Ile Glu Thr Ile Ile

 20  1               5                   10                  15

     Asn Thr Phe His Gln Tyr Ser Val Lys Leu Gly His Pro Asp Thr Leu

                 20                  25                  30

     Asn Gln Gly Glu Phe Lys Glu Leu Val Arg Lys Asp Leu Gln Asn Phe

             35                  40                  45
```

Leu Lys Lys Glu Asn Lys Asn Glu Lys Val Ile Glu His Ile Met Glu

      50   55   60

Asp Leu Asp Thr Asn Ala Asp Lys Gln Leu Ser Phe Glu Glu Phe Ile

      65   70   75   80

5   Met Leu Met Ala Arg Leu Thr Trp Ala Ser His Glu Lys Met His Glu

               85   90   95

Gly Asp Glu Gly Pro Gly His His His Lys Pro Gly Leu Gly Glu Gly

           100   105   110

Thr Pro

10

<210>   50

<211>   348

15 <212>   PRT

<213>   Homo sapiens

<220>.

<221>   Macrophage capping protein

<222>   (1)..(348)

20 <223>   Accession No. as of 10 Dec 2002: P40121

<400>   50

Met Tyr Thr Ala Ile Pro Gln Ser Gly Ser Pro Phe Pro Gly Ser Val

      1   5   10   15

```
    Gln Asp Pro Gly Leu His Val Trp Arg Val Glu Lys Leu Lys Pro Val
                    20                  25                  30

    Pro Val Ala Gln Glu Asn Gln Gly Val Phe Phe Ser Gly Asp Ser Tyr
                    35                  40                  45

 5  Leu Val Leu His Asn Gly Pro Glu Glu Val Ser His Leu His Leu Trp
                    50                  55                  60

    Ile Gly Gln Gln Ser Ser Arg Asp Glu Gln Gly Ala Cys Ala Val Leu
    65                  70                  75                  80

    Ala Val His Leu Asn Thr Leu Leu Gly Glu Arg Pro Val Gln His Arg
10                  85                  90                  95

    Glu Val Gln Gly Asn Glu Ser Asp Leu Phe Met Ser Tyr Phe Pro Arg
                    100                 105                 110

    Gly Leu Lys Tyr Gln Glu Gly Gly Val Glu Ser Ala Phe His Lys Thr
                    115                 120                 125

15  Ser Thr Gly Ala Pro Ala Ala Ile Lys Lys Leu Tyr Gln Val Lys Gly
                    130                 135                 140

    Lys Lys Asn Ile Arg Ala Thr Glu Arg Ala Leu Asn Trp Asp Ser Phe
    145                 150                 155                 160

    Asn Thr Gly Asp Cys Phe Ile Leu Asp Leu Gly Gln Asn Ile Phe Ala
20                  165                 170                 175

    Trp Cys Gly Gly Lys Ser Asn Ile Leu Glu Arg Asn Lys Ala Arg Asp
                    180                 185                 190

    Leu Ala Leu Ala Ile Arg Asp Ser Glu Arg Gln Gly Lys Ala Gln Val
                    195                 200                 205
```

Glu Ile Val Thr Asp Gly Glu Glu Pro Ala Glu Met Ile Gln Val Leu
          210   215   220

Gly Pro Lys Pro Ala Leu Lys Glu Gly Asn Pro Glu Glu Asp Leu Thr

225   230   235   240

5   Ala Asp Lys Ala Asn Ala Gln Ala Ala Ala Leu Tyr Lys Val Ser Asp
                    245   250   255

    Ala Thr Gly Gln Met Asn Leu Thr Lys Val Ala Asp Ser Ser Pro Phe
                    260   265   270

    Ala Leu Glu Leu Leu Ile Ser Asp Asp Cys Phe Val Leu Asp Asn Gly

10   275   280   285

    Leu Cys Gly Lys Ile Tyr Ile Trp Lys Gly Arg Lys Ala Asn Glu Lys
                290   295   300

    Glu Arg Gln Ala Ala Leu Gln Val Ala Glu Gly Phe Ile Ser Arg Met

    305   310   315   320

15 Gln Tyr Ala Pro Asn Thr Gln Val Glu Ile Leu Pro Gln Gly Arg Glu
                    325   330   335

    Ser Pro Ile Phe Lys Gln Phe Phe Lys Asp Trp Lys
                    340   345

        ⁄

20

    <210> 51

    <211> 346

    <212> PRT

    <213> Homo sapiens

<220>

<221>   Annexin I

<222>   (1)..(346)

<223>   Accession No. as of 10 Dec 2002: P04083

5   <400>   51

Met Ala Met Val Ser Glu Phe Leu Lys Gln Ala Trp Phe Ile Glu Asn
1   5   10   15

Glu Glu Gln Glu Tyr Val Gln Thr Val Lys Ser Ser Lys Gly Gly Pro
10   20   25   30

Gly Ser Ala Val Ser Pro Tyr Pro Thr Phe Asn Pro Ser Ser Asp Val
                35   40   45

Ala Ala Leu His Lys Ala Ile Met Val Lys Gly Val Asp Glu Ala Thr
                50   55   60

15 Ile Ile Asp Ile Leu Thr Lys Arg Asn Asn Ala Gln Arg Gln Gln Ile
    65   70   75   80

Lys Ala Ala Tyr Leu Gln Glu Thr Gly Lys Pro Leu Asp Glu Thr Leu
                85   90   95

Lys Lys Ala Leu Thr Gly His Leu Glu Glu Val Val Leu Ala Leu Leu
20   100   105   110

Lys Thr Pro Ala Gln Phe Asp Ala Asp Glu Leu Arg Ala Ala Met Lys
                115   120   125

Gly Leu Gly Thr Asp Glu Asp Thr Leu Ile Glu Ile Leu Ala Ser Arg
                130   135   140

Thr Asn Lys Glu Ile Arg Asp Ile Asn Arg Val Tyr Arg Glu Glu Leu

145   150   155   160

Lys Arg Asp Leu Ala Lys Asp Ile Thr Ser Asp Thr Ser Gly Asp Phe

           165   170   175

5   Arg Asn Ala Leu Leu Ser Leu Ala Lys Gly Asp Arg Ser Glu Asp Phe

           180   185   190

Gly Val Asn Glu Asp Leu Ala Asp Ser Asp Ala Arg Ala Leu Tyr Glu

           195   200   205

Ala Gly Glu Arg Arg Lys Gly Thr Asp Val Asn Val Phe Asn Thr Ile

10   210   215   220

Leu Thr Thr Arg Ser Tyr Pro Gln Leu Arg Arg Val Phe Gln Lys Tyr

225   230   235   240

Thr Lys Tyr Ser Lys His Asp Met Asn Lys Val Leu Asp Leu Glu Leu

           245   250   255

15   Lys Gly Asp Ile Glu Lys Cys Leu Thr Ala Ile Val Lys Cys Ala Thr

           260   265   270

Ser Lys Pro Ala Phe Phe Ala Glu Lys Leu His Gln Ala Met Lys Gly

           275   280   285

Val Gly Thr Arg His Lys Ala Leu Ile Arg Ile Met Val Ser Arg Ser

20   290   295   300

Glu Ile Asp Met Asn Asp Ile Lys Ala Phe Tyr Gln Lys Met Tyr Gly

305   310   315   320

Ile Ser Leu Cys Gln Ala Ile Leu Asp Glu Thr Lys Gly Asp Tyr Glu

           325   330   335

Lys Ile Leu Val Ala Leu Cys Gly Gly Asn

                340   345

5   <210> 52

     <211> 469

     <212> PRT

     <213> Homo sapiens

     <220>

10   <221> Keratin, type II cytoskeletal 7

     <222> (1)..(469)

     <223> Accession No. as of 10 Dec 2002: P08729

     <400> 52

15   Met Ser Ile His Phe Ser Ser Pro Val Phe Thr Ser Arg Ser Ala Ala

     1   5   10   15

     Phe Ser Gly Arg Gly Ala Gln Val Arg Leu Ser Ser Ala Arg Pro Gly

                    20   25   30

     Gly Leu Gly Ser Ser Ser Leu Tyr Gly Leu Gly Ala Ser Arg Pro Arg

20   35   40   45

     Val Ala Val Arg Ser Ala Tyr Gly Gly Pro Val Gly Ala Gly Ile Arg

                50   55   60

     Glu Val Thr Ile Asn Gln Ser Leu Leu Ala Pro Leu Arg Leu Asp Ala

     65   70   75   80

Asp Pro Ser Leu Gln Arg Val Arg Gln Glu Glu Ser Glu Gln Ile Lys

                    85   90   95

Thr Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu

                   100   105   110

5   Glu Gln Gln Asn Lys Leu Leu Glu Thr Lys Trp Thr Leu Leu Gln Glu

                   115   120   125

Gln Lys Ser Ala Lys Ser Ser Arg Leu Pro Asp Ile Phe Glu Ala Gln

                   130   135   140

Ile Ala Gly Leu Arg Gly Gln Leu Glu Ala Leu Gln Val Asp Gly Gly

10   145   150   155   160

Arg Leu Glu Gln Gly Leu Arg Thr Met Gln Asp Val Val Glu Asp Phe

                   165   170   175

Lys Asn Lys Tyr Glu Asp Glu Ile Asn Arg Arg Thr Ala Ala Glu Asn

                   180   185   190

15   Glu Phe Val Val Leu Lys Lys Asp Val Asp Ala Ala Tyr Met Ser Lys

                   195   200   205

Val Glu Leu Glu Ala Lys Val Asp Ala Leu Asn Asp Glu Ile Asn Phe

                   210   215   220

Leu Arg Thr Leu Asn Glu Thr Glu Leu Thr Glu Leu Gln Ser Gln Ile

20   225   230   235   240

Ser Asp Thr Ser Val Val Leu Ser Met Asp Asn Ser Arg Ser Leu Asp

                   245   250   255

Leu Asp Gly Ile Ile Ala Glu Val Lys Ala Gln Tyr Glu Glu Met Ala

                   260   265   270

Lys Cys Ser Arg Ala Glu Ala Glu Ala Trp Tyr Gln Thr Lys Phe Glu
            275   280   285

Thr Leu Gln Ala Gln Ala Gly Lys His Gly Asp Asp Leu Arg Asn Thr
            290   295   300

5 Arg Asn Glu Ile Ser Glu Met Asn Arg Ala Ile Gln Arg Leu Gln Ala
       305   310   315   320

Glu Ile Asp Asn Ile Lys Asn Gln Arg Ala Lys Leu Glu Ala Ala Ile
                325   330   335

Ala Glu Ala Glu Glu Arg Gly Glu Leu Ala Leu Lys Asp Ala Arg Ala
10   340   345   350

Lys Gln Glu Glu Leu Glu Ala Ala Leu Gln Arg Ala Lys Gln Asp Met
            355   360   365

Ala Arg Gln Leu Arg Glu Tyr Gln Glu Leu Met Ser Val Lys Leu Ala
            370   375   380

15 Leu Asp Ile Glu Ile Ala Thr Tyr Arg Lys Leu Leu Glu Gly Glu Glu
       385   390   395   400

Ser Arg Leu Ala Gly Asp Gly Val Gly Ala Val Asn Ile Ser Val Met
                405   410   415

Asn Ser Thr Gly Gly Ser Ser Ser Gly Gly Gly Ile Gly Leu Thr Leu
20   420   425   430

Gly Gly Thr Met Gly Ser Asn Ala Leu Ser Phe Ser Ser Ser Ala Gly
            435   440   445

Pro Gly Leu Leu Lys Ala Tyr Ser Ile Arg Thr Ala Ser Ala Ser Arg
            450   455   460

Arg Ser Ala Arg Asp

465

5   <210>   53

    <211>   836

    <212>   PRT

    <213>   Homo sapiens

    <220>

10 <221>   Osteoblast specific factor 2 precursor

    <222>   (1)..(836)

    <223>   Accession No. as of 10 Dec 2002: Q15063

    <400>   53

15 Met Ile Pro Phe Leu Pro Met Phe Ser Leu Leu Leu Leu Leu Ile Val

    1   5   10   15

    Asn Pro Ile Asn Ala Asn Asn His Tyr Asp Lys Ile Leu Ala His Ser

                    20   25   30

    Arg Ile Arg Gly Arg Asp Gln Gly Pro Asn Val Cys Ala Leu Gln Gln

20   35   40   45

    Ile Leu Gly Thr Lys Lys Lys Tyr Phe Ser Thr Cys Lys Asn Trp Tyr

            50   55   60

    Lys Lys Ser Ile Cys Gly Gln Lys Thr Thr Val Leu Tyr Glu Cys Cys

    65   70   75   80

Pro Gly Tyr Met Arg Met Glu Gly Met Lys Gly Cys Pro Ala Val Leu

                    85   90   95

Pro Ile Asp His Val Tyr Gly Thr Leu Gly Ile Val Gly Ala Thr Thr

                    100   105   110

5   Thr Gln Arg Tyr Ser Asp Ala Ser Lys Leu Arg Glu Glu Ile Glu Gly

                    115   120   125

Lys Gly Ser Phe Thr Tyr Phe Ala Pro Ser Asn Glu Ala Trp Asp Asn

                    130   135   140

Leu Asp Ser Asp Ile Arg Arg Gly Leu Glu Ser Asn Val Asn Val Glu

10 145   150   155   160

Leu Leu Asn Ala Leu His Ser His Met Ile Asn Lys Arg Met Leu Thr

                    165   170   175

Lys Asp Leu Lys Asn Gly Met Ile Ile Pro Ser Met Tyr Asn Asn Leu

                    180   185   190

15 Gly Leu Phe Ile Asn His Tyr Pro Asn Gly Val Val Thr Val Asn Cys

                    195   200   205

Ala Arg Ile Ile His Gly Asn Gln Ile Ala Thr Asn Gly Val Val His

                    210   215   220

Val Ile Asp Arg Val Leu Thr Gln Ile Gly Thr Ser Ile Gln Asp Phe

20 225   230   235   240

Ile Glu Ala Glu Asp Asp Leu Ser Ser Phe Arg Ala Ala Ala Ile Thr

                    245   250   255

Ser Asp Ile Leu Glu Ala Leu Gly Arg Asp Gly His Phe Thr Leu Phe

                    260   265   270

```
      Ala Pro Thr Asn Glu Ala Phe Glu Lys Leu Pro Arg Gly Val Leu Glu
              275                 280                 285

      Arg Phe Met Gly Asp Lys Val Ala Ser Glu Ala Leu Met Lys Tyr His
              290                 295                 300

  5   Ile Leu Asn Thr Leu Gln Cys Ser Glu Ser Ile Met Gly Gly Ala Val
      305                 310                 315                 320

      Phe Glu Thr Leu Glu Gly Asn Thr Ile Glu Ile Gly Cys Asp Gly Asp
                          325                 330                 335

      Ser Ile Thr Val Asn Gly Ile Lys Met Val Asn Lys Lys Asp Ile Val
 10                       340                 345                 350

      Thr Asn Asn Gly Val Ile His Leu Ile Asp Gln Val Leu Ile Pro Asp
                  355                 360                 365

      Ser Ala Lys Gln Val Ile Glu Leu Ala Gly Lys Gln Gln Thr Thr Phe
                  370                 375                 380

 15   Thr Asp Leu Val Ala Gln Leu Gly Leu Ala Ser Ala Leu Arg Pro Asp
      385                 390                 395                 400

      Gly Glu Tyr Thr Leu Leu Ala Pro Val Asn Asn Ala Phe Ser Asp Asp
                          405                 410                 415

      Thr Leu Ser Met Val Gln Arg Leu Leu Lys Leu Ile Leu Gln Asn His
 20                       420                 425                 430

      Ile Leu Lys Val Lys Val Gly Leu Asn Glu Leu Tyr Asn Gly Gln Ile
                      435                 440                 445

      Leu Glu Thr Ile Gly Gly Lys Gln Leu Arg Val Phe Val Tyr Arg Thr
                  450                 455                 460
```

Ala Val Cys Ile Glu Asn Ser Cys Met Glu Lys Gly Ser Lys Gln Gly
   465   470   475   480

Arg Asn Gly Ala Ile His Ile Phe Arg Glu Ile Ile Lys Pro Ala Glu
            485   490   495

5 Lys Ser Leu His Glu Lys Leu Lys Gln Asp Lys Arg Phe Ser Thr Phe
          500   505   510

Leu Ser Leu Leu Glu Ala Ala Asp Leu Lys Glu Leu Leu Thr Gln Pro
        515   520   525

Gly Asp Trp Thr Leu Phe Val Pro Thr Asn Asp Ala Phe Lys Gly Met
10   530   535   540

Thr Ser Glu Glu Lys Glu Ile Leu Ile Arg Asp Lys Asn Ala Leu Gln
545   550   555   560

Asn Ile Ile Leu Tyr His Leu Thr Pro Gly Val Phe Ile Gly Lys Gly
        565   570   575

15 Phe Glu Pro Gly Val Thr Asn Ile Leu Lys Thr Thr Gln Gly Ser Lys
        580   585   590

Ile Phe Leu Lys Glu Val Asn Asp Thr Leu Leu Val Asn Glu Leu Lys
        595   600   605

Ser Lys Glu Ser Asp Ile Met Thr Thr Asn Gly Val Ile His Val Val
20   610   615   620

Asp Lys Leu Leu Tyr Pro Ala Asp Thr Pro Val Gly Asn Asp Gln Leu
625   630   635   640

Leu Glu Ile Leu Asn Lys Leu Ile Lys Tyr Ile Gln Ile Lys Phe Val
        645   650   655

Arg Gly Ser Thr Phe Lys Glu Ile Pro Val Thr Val Tyr Thr Thr Lys

660   665   670

Ile Ile Thr Lys Val Val Glu Pro Lys Ile Lys Val Ile Glu Gly Ser

675   680   685

5   Leu Gln Pro Ile Ile Lys Thr Glu Gly Pro Thr Leu Thr Lys Val Lys

690   695   700

Ile Glu Gly Glu Pro Glu Phe Arg Leu Ile Lys Glu Gly Glu Thr Ile

705   710   715   720

Thr Glu Val Ile His Gly Glu Pro Ile Ile Lys Lys Tyr Thr Lys Ile

10   725   730   735

Ile Asp Gly Val Pro Val Glu Ile Thr Glu Lys Glu Thr Arg Glu Glu

740   745   750

Arg Ile Ile Thr Gly Pro Glu Ile Lys Tyr Thr Arg Ile Ser Thr Gly

755   760   765

15   Gly Gly Glu Thr Glu Glu Thr Leu Lys Lys Leu Leu Gln Glu Glu Val

770   775   780

Thr Lys Val Thr Lys Phe Ile Glu Gly Gly Asp Gly His Leu Phe Glu

785   790   795   800

Asp Glu Glu Ile Lys Arg Leu Leu Gln Gly Asp Thr Pro Val Arg Lys

20   805   810   815

Leu Gln Ala Asn Lys Lys Val Gln Gly Ser Arg Arg Arg Leu Arg Glu

820   825   830

Gly Arg Ser Gln

835

<210> 54

<211> 687

5   <212> PRT

<213> Homo sapiens

<220>

<221> Protein-glutamine gamma-glutamyltransferase

<222> (1)..(687)

10   <223> Accession No. P21980

<400> 54

Met Ala Glu Glu Leu Val Leu Glu Arg Cys Asp Leu Glu Leu Glu Thr

1   5   10   15

15 Asn Gly Arg Asp His His Thr Ala Asp Leu Cys Arg Glu Lys Leu Val

               20   25   30

Val Arg Arg Gly Gln Pro Phe Trp Leu Thr Leu His Phe Glu Gly Arg

               35   40   45

Asn Tyr Glu Ala Ser Val Asp Ser Leu Thr Phe Ser Val Val Thr Gly

20   50   55   60

Pro Ala Pro Ser Gln Glu Ala Gly Thr Lys Ala Arg Phe Pro Leu Arg

65   70   75   80

Asp Ala Val Glu Glu Gly Asp Trp Thr Ala Thr Val Val Asp Gln Gln

               85   90   95

Asp Cys Thr Leu Ser Leu Gln Leu Thr Thr Pro Ala Asn Ala Pro Ile
              100   105   110

Gly Leu Tyr Arg Leu Ser Leu Glu Ala Ser Thr Gly Tyr Gln Gly Ser
              115   120   125

5   Ser Phe Val Leu Gly His Phe Ile Leu Leu Phe Asn Ala Trp Cys Pro
              130   135   140

Ala Asp Ala Val Tyr Leu Asp Ser Glu Glu Glu Arg Gln Glu Tyr Val
     145   150   155   160

Leu Thr Gln Gln Gly Phe Ile Tyr Gln Gly Ser Ala Lys Phe Ile Lys
10   165   170   175

Asn Ile Pro Trp Asn Phe Gly Gln Phe Glu Asp Gly Ile Leu Asp Ile
              180   185   190

Cys Leu Ile Leu Leu Asp Val Asn Pro Lys Phe Leu Lys Asn Ala Gly
              195   200   205

15   Arg Asp Cys Ser Arg Arg Ser Ser Pro Val Tyr Val Gly Arg Val Val
              210   215   220

Ser Gly Met Val Asn Cys Asn Asp Asp Gln Gly Val Leu Leu Gly Arg
     225   230   235   240

Trp Asp Asn Asn Tyr Gly Asp Gly Val Ser Pro Met Ser Trp Ile Gly
20   245   250   255

Ser Val Asp Ile Leu Arg Arg Trp Lys Asn His Gly Cys Gln Arg Val
              260   265   270

Lys Tyr Gly Gln Cys Trp Val Phe Ala Ala Val Ala Cys Thr Val Leu
              275   280   285

        Arg Cys Leu Gly Ile Pro Thr Arg Val Val Thr Asn Tyr Asn Ser Ala
            290   295   300

        His Asp Gln Asn Ser Asn Leu Leu Ile Glu Tyr Phe Arg Asn Glu Phe
        305   310   315   320

    5   Gly Glu Ile Gln Gly Asp Lys Ser Glu Met Ile Trp Asn Phe His Cys
                        325   330   335

        Trp Val Glu Ser Trp Met Thr Arg Pro Asp Leu Gln Pro Gly Tyr Glu
                        340   345   350

        Gly Trp Gln Ala Leu Asp Pro Thr Pro Gln Glu Lys Ser Glu Gly Thr
    10   355   360   365

        Tyr Cys Cys Gly Pro Val Pro Val Arg Ala Ile Lys Glu Gly Asp Leu
                        370   375   380

        Ser Thr Lys Tyr Asp Ala Pro Phe Val Phe Ala Glu Val Asn Ala Asp
        385   390   395   400

    15 Val Val Asp Trp Ile Gln Gln Asp Asp Gly Ser Val His Lys Ser Ile
                        405   410   415

        Asn Arg Ser Leu Ile Val Gly Leu Lys Ile Ser Thr Lys Ser Val Gly
                        420   425   430

        Arg Asp Glu Arg Glu Asp Ile Thr His Thr Tyr Lys Tyr Pro Glu Gly
    20   435   440   445

        Ser Ser Glu Glu Arg Glu Ala Phe Thr Arg Ala Asn His Leu Asn Lys
                        450   455   460

        Leu Ala Glu Lys Glu Glu Thr Gly Met Ala Met Arg Ile Arg Val Gly
        465   470   475   480

Gln Ser Met Asn Met Gly Ser Asp Phe Asp Val Phe Ala His Ile Thr

485   490   495

Asn Asn Thr Ala Glu Glu Tyr Val Cys Arg Leu Leu Leu Cys Ala Arg

500   505   510

5   Thr Val Ser Tyr Asn Gly Ile Leu Gly Pro Glu Cys Gly Thr Lys Tyr

515   520   525

Leu Leu Asn Leu Asn Leu Glu Pro Phe Ser Glu Lys Ser Val Pro Leu

530   535   540

Cys Ile Leu Tyr Glu Lys Tyr Arg Asp Cys Leu Thr Glu Ser Asn Leu

10 545   550   555   560

Ile Lys Val Arg Ala Leu Leu Val Glu Pro Val Ile Asn Ser Tyr Leu

565   570   575

Leu Ala Glu Arg Asp Leu Tyr Leu Glu Asn Pro Glu Ile Lys Ile Arg

580   585   590

15 Ile Leu Gly Glu Pro Lys Gln Lys Arg Lys Leu Val Ala Glu Val Ser

595   600   605

Leu Gln Asn Pro Leu Pro Val Ala Leu Glu Gly Cys Thr Phe Thr Val

610   615   620

Glu Gly Ala Gly Leu Thr Glu Glu Gln Lys Thr Val Glu Ile Pro Asp

20 625   630   635   640

Pro Val Glu Ala Gly Glu Glu Val Lys Val Arg Met Asp Leu Leu Pro

645   650   655

Leu His Met Gly Leu His Lys Leu Val Val Asn Phe Glu Ser Asp Lys

660   665   670

Leu Lys Ala Val Lys Gly Phe Arg Asn Val Ile Ile Gly Pro Ala

        675   680   685

5   <210> 55

    <211> 204

    <212> PRT

    <213> Homo sapiens

    <220>

10 <221> Rho GDP-dissociation inhibitor 1

    <222> (1)..(204)

    <223> Accession No. as of 10 Dec 2002: P52565

    <400> 55

15 Met Ala Glu Gln Glu Pro Thr Ala Glu Gln Leu Ala Gln Ile Ala Ala

    1   5   10   15

    Glu Asn Glu Glu Asp Glu His Ser Val Asn Tyr Lys Pro Pro Ala Gln

                20   25   30

    Lys Ser Ile Gln Glu Ile Gln Glu Leu Asp Lys Asp Asp Glu Ser Leu

20   35   40   45

    Arg Lys Tyr Lys Glu Ala Leu Leu Gly Arg Val Ala Val Ser Ala Asp

            50   55   60

    Pro Asn Val Pro Asn Val Val Val Thr Gly Leu Thr Leu Val Cys Ser

    65   70   75   80

Ser Ala Pro Gly Pro Leu Glu Leu Asp Leu Thr Gly Asp Leu Glu Ser
                85   90   95

Phe Lys Lys Gln Ser Phe Val Leu Lys Glu Gly Val Glu Tyr Arg Ile
                100   105   110

5 Lys Ile Ser Phe Arg Val Asn Arg Glu Ile Val Ser Gly Met Lys Tyr
                115   120   125

Ile Gln His Thr Tyr Arg Lys Gly Val Lys Ile Asp Lys Thr Asp Tyr
            130   135   140

Met Val Gly Ser Tyr Gly Pro Arg Ala Glu Glu Tyr Glu Phe Leu Thr
10 145   150   155   160

Pro Val Glu Glu Ala Pro Lys Gly Met Leu Ala Arg Gly Ser Tyr Ser
                165   170   175

Ile Lys Ser Arg Phe Thr Asp Asp Asp Lys Thr Asp His Leu Ser Trp
                180   185   190

15 Glu Trp Asn Leu Thr Ile Lys Lys Asp Trp Lys Asp
                195   200

    <210> 56

20 <211> 492

    <212> PRT

    <213> Homo sapiens

    <220>

    <221> Fascin 2

<222>   (1)..(492)

<223>   Accession No. as of 29 August 2003: O14926

<400>   56

5   Met Pro Thr Asn Gly Leu His Gln Val Leu Lys Ile Gln Phe Gly Leu

     1   5   10   15

     Val Asn Asp Thr Asp Arg Tyr Leu Thr Ala Glu Ser Phe Gly Phe Lys

                     20   25   30

     Val Asn Ala Ser Ala Pro Ser Leu Lys Arg Lys Gln Thr Trp Val Leu

10   35   40   45

     Glu Pro Asp Pro Gly Gln Gly Thr Ala Val Leu Leu Arg Ser Ser His

                 50   55   60

     Leu Gly Arg Tyr Leu Ser Ala Glu Glu Asp Gly Arg Val Ala Cys Glu

     65   70   75   80

15   Ala Glu Gln Pro Gly Arg Asp Cys Arg Phe Leu Val Leu Pro Gln Pro

                         85   90   95

     Asp Gly Arg Trp Val Leu Arg Ser Glu Pro His Gly Arg Phe Phe Gly

                     100   105   110

     Gly Thr Glu Asp Gln Leu Ser Cys Phe Ala Thr Ala Val Ser Pro Ala

20   115   120   125

     Glu Leu Trp Thr Val His Leu Ala Ile His Pro Gln Ala His Leu Leu

                 130   135   140

     Ser Val Ser Arg Arg Arg Tyr Val His Leu Cys Pro Arg Glu Asp Glu

     145   150   155   160

Met Ala Ala Asp Gly Asp Lys Pro Trp Gly Val Asp Ala Leu Leu Thr
                165   170   175

Leu Ile Phe Arg Ser Arg Arg Tyr Cys Leu Lys Ser Cys Asp Ser Arg
                180   185   190

5   Tyr Leu Arg Ser Asp Gly Arg Leu Val Trp Glu Pro Glu Pro Arg Ala
            - 195   200   205

    Cys Tyr Thr Leu Glu Phe Lys Ala Gly Lys Leu Ala Phe Lys Asp Cys
            210   215   220

    Asp Gly His Tyr Leu Ala Pro Val Gly Pro Ala Gly Thr Leu Lys Ala
10 225   230   235   240

    Gly Arg Asn Thr Arg Pro Gly Lys Asp Glu Leu Phe Asp Leu Glu Glu
                245   250   255

    Ser His Pro Gln Val Val Leu Val Ala Ala Asn His Arg Tyr Val Ser
                260   265   270

15 Val Arg Gln Gly Val Asn Val Ser Ala Asn Gln Asp Asp Glu Leu Asp
                275   280   285

    His Glu Thr Phe Leu Met Gln Ile Asp Gln Glu Thr Lys Lys Cys Thr
                290   295   300

    Phe Tyr Ser Ser Thr Gly Gly Tyr Trp Thr Leu Val Thr His Gly Gly
20 305   310   315   320

    Ile His Ala Thr Ala Thr Gln Val Ser Ala Asn Thr Met Phe Glu Met
                325   330   335

    Glu Trp Arg Gly Arg Arg Val Ala Leu Lys Ala Ser Asn Gly Arg Tyr
                340   345   350

Val Cys Met Lys Lys Asn Gly Gln Leu Ala Ala Ile Ser Asp Phe Val
355 360 365

Gly Lys Asp Glu Glu Phe Thr Leu Lys Leu Ile Asn Arg Pro Ile Leu
370 375 380

5   Val Leu Arg Gly Leu Asp Gly Phe Val Cys His His Arg Gly Ser Asn
385 390 395 400

Gln Leu Asp Thr Asn Arg Ser Val Tyr Asp Val Phe His Leu Ser Phe
405 410 415

Ser Asp Gly Ala Tyr Arg Ile Arg Gly Arg Asp Gly Gly Phe Trp Tyr
10   420 425 430

Thr Gly Ser His Gly Ser Val Cys Ser Asp Gly Glu Arg Ala Glu Asp
435 440 445

Phe Val Phe Glu Phe Arg Glu Arg Gly Arg Leu Ala Ile Arg Ala Arg
450 455 460

15   Ser Gly Lys Tyr Leu Arg Gly Gly Ala Ser Gly Leu Leu Arg Ala Asp
465 470 475 480

Ala Asp Ala Pro Ala Gly Thr Ala Leu Trp Glu Tyr
485 490

20

<210> 57

<211> 165

<212> PRT

<213> Homo sapiens

<220>

<221> Destrin (Actin-depolymerizing factor) (ADF)

<222> (1)..(165)

<223> Accession No. as of 29 August 2003: P18282

<400> 57

Met Ala Ser Gly Val Gln Val Ala Asp Glu Val Cys Arg Ile Phe Tyr
1   5   10   15

Asp Met Lys Val Arg Lys Cys Ser Thr Pro Glu Glu Ile Lys Lys Arg
            20   25   30

Lys Lys Ala Val Ile Phe Cys Leu Ser Ala Asp Lys Lys Cys Ile Ile
        35   40   45

Val Glu Glu Gly Lys Glu Ile Leu Val Gly Asp Val Gly Val Thr Ile
        50   55   60

Thr Asp Pro Phe Lys His Phe Val Gly Met Leu Pro Glu Lys Asp Cys
65   70   75   80

Arg Tyr Ala Leu Tyr Asp Ala Ser Phe Glu Thr Lys Glu Ser Arg Lys
                85   90   95

Glu Glu Leu Met Phe Phe Leu Trp Ala Pro Glu Leu Ala Pro Leu Lys
                100   105   110

Ser Lys Met Ile Tyr Ala Ser Ser Lys Asp Ala Ile Lys Lys Lys Phe
                115   120   125

Gln Gly Ile Lys His Glu Cys Gln Ala Asn Gly Pro Glu Asp Leu Asn
            130   135   140

Arg Ala Cys Ile Ala Glu Lys Leu Gly Gly Ser Leu Ile Val Ala Phe

145   150   155   160

Glu Gly Cys Pro Val

                    165

5

<210> 58

<211> 492

<212> PRT

10 <213> Homo sapiens

<220>

<221> Fascin

<222> (1)..(492)

<223> Accession No. as of 29 August 2003: Q16658

15 <400> 58

Thr Ala Asn Gly Thr Ala Glu Ala Val Gln Ile Gln Phe Gly Leu Ile

1   5   10   15

Asn Cys Gly Asn Lys Tyr Leu Thr Ala Glu Ala Phe Gly Phe Lys Val

20   20   25   30

Asn Ala Ser Ala Ser Ser Leu Lys Lys Lys Gln Ile Trp Thr Leu Glu

                35   40   45

Gln Pro Pro Asp Glu Ala Gly Ser Ala Ala Val Cys Leu Arg Ser His

        50   55   60

```
     Leu Gly Arg Tyr Leu Ala Ala Asp Lys Asp Gly Asn Val Thr Cys Glu
     65              70              75              80

     Arg Glu Val Pro Gly Pro Asp Cys Arg Phe Leu Ile Val Ala His Asp
                     85              90              95

 5   Asp Gly Arg Trp Ser Leu Gln Ser Glu Ala His Arg Arg Tyr Phe Gly
                     100             105             110

     Gly Thr Glu Asp Arg Leu Ser Cys Phe Ala Gln Thr Val Ser Pro Ala
                     115             120             125

     Glu Lys Trp Ser Val His Ile Ala Met His Pro Gln Val Asn Ile Tyr
10         130             135             140

     Ser Val Thr Arg Lys Arg Tyr Ala His Leu Ser Ala Arg Pro Ala Asp
     145             150             155             160

     Glu Ile Ala Val Asp Arg Asp Val Pro Trp Gly Val Asp Ser Leu Ile
                     165             170             175

15   Thr Leu Ala Phe Gln Asp Gln Arg Tyr Ser Val Gln Thr Ala Asp His
                     180             185             190

     Arg Phe Leu Arg His Asp Gly Arg Leu Val Ala Arg Pro Glu Pro Ala
                     195             200             205

     Thr Gly Tyr Thr Leu Glu Phe Arg Ser Gly Lys Val Ala Phe Arg Asp
20         210             215             220

     Cys Glu Gly Arg Tyr Leu Ala Pro Ser Gly Pro Ser Gly Thr Leu Lys
     225             230             235             240

     Ala Gly Lys Ala Thr Lys Val Gly Lys Asp Glu Leu Phe Ala Leu Glu
                     245             250             255
```

Gln Ser Cys Ala Gln Val Val Leu Gln Ala Ala Asn Glu Arg Asn Val
             260   265   270

Ser Thr Arg Gln Gly Met Asp Leu Ser Ala Asn Gln Asp Glu Glu Thr
             275   280   285

5   Asp Gln Glu Thr Phe Gln Leu Glu Ile Asp Arg Asp Thr Lys Lys Cys
             290   295   300

Ala Phe Arg Thr His Thr Gly Lys Tyr Trp Thr Leu Thr Ala Thr Gly
     305   310   315   320

Gly Val Gln Ser Thr Ala Ser Ser Lys Asn Ala Ser Cys Tyr Phe Asp
10   325   330   335

Ile Glu Trp Arg Asp Arg Arg Ile Thr Leu Arg Ala Ser Asn Gly Lys
             340   345   350

Phe Val Thr Ser Lys Lys Asn Gly Gln Leu Ala Ala Ser Val Glu Thr
             355   360   365

15 Ala Gly Asp Ser Glu Leu Phe Leu Met Lys Leu Ile Asn Arg Pro Ile
             370   375   380

Ile Val Phe Arg Gly Glu His Gly Phe Ile Gly Cys Arg Lys Val Thr
     385   390   395   400

Gly Thr Leu Asp Ala Asn Arg Ser Ser Tyr Asp Val Phe Gln Leu Glu
20   405   410   415

Phe Asn Asp Gly Ala Tyr Asn Ile Lys Asp Ser Thr Gly Lys Tyr Trp
             420   425   430

Thr Val Gly Ser Asp Ser Ala Val Thr Ser Ser Gly Asp Thr Pro Val
             435   440   445

Asp Phe Phe Phe Glu Phe Cys Asp Tyr Asn Lys Val Ala Ile Lys Val

        450   455   460

Gly Gly Arg Tyr Leu Lys Gly Asp His Ala Gly Val Leu Lys Ala Ser

        465   470   475   480

5   Ala Glu Thr Val Asp Pro Ala Ser Leu Trp Glu Tyr

            485   490

        <210>   59

10 <211>   317

    <212>   PRT

    <213>   Homo sapiens

    <220>

    <221>   Apo-E precursor

15 <222>   (1)..(317)

    <223>   Accession No. as of 29 August 2003: P02649

    <400>   59

    Met Lys Val Leu Trp Ala Ala Leu Leu Val Thr Phe Leu Ala Gly Cys

20 1   5   10   15

    Gln Ala Lys Val Glu Gln Ala Val Glu Thr Glu Pro Glu Pro Glu Leu

                20   25   30

    Arg Gln Gln Thr Glu Trp Gln Ser Gly Gln Arg Trp Glu Leu Ala Leu

                35   40   45

Gly Arg Phe Trp Asp Tyr Leu Arg Trp Val Gln Thr Leu Ser Glu Gln

     50   55   60

Val Gln Glu Glu Leu Leu Ser Ser Gln Val Thr Gln Glu Leu Arg Ala

     65   70   75   80

5   Leu Met Asp Glu Thr Met Lys Glu Leu Lys Ala Tyr Lys Ser Glu Leu

           85   90   95

Glu Glu Gln Leu Thr Pro Val Ala Glu Glu Thr Arg Ala Arg Leu Ser

          100   105   110

Lys Glu Leu Gln Ala Ala Gln Ala Arg Leu Gly Ala Asp Met Glu Asp

10   115   120   125

Val Cys Gly Arg Leu Val Gln Tyr Arg Gly Glu Val Gln Ala Met Leu

      130   135   140

Gly Gln Ser Thr Glu Glu Leu Arg Val Arg Leu Ala Ser His Leu Arg

    145   150   155   160

15 Lys Leu Arg Lys Arg Leu Leu Arg Asp Ala Asp Asp Leu Gln Lys Arg

          165   170   175

Leu Ala Val Tyr Gln Ala Gly Ala Arg Glu Gly Ala Glu Arg Gly Leu

        180   185   190

Ser Ala Ile Arg Glu Arg Leu Gly Pro Leu Val Glu Gln Gly Arg Val

20   195   200   205

Arg Ala Ala Thr Val Gly Ser Leu Ala Gly Gln Pro Leu Gln Glu Arg

     210   215   220

Ala Gln Ala Trp Gly Glu Arg Leu Arg Ala Arg Met Glu Glu Met Gly

225   230   235   240

Ser Arg Thr Arg Asp Arg Leu Asp Glu Val Lys Glu Gln Val Ala Glu

            245   250   255

Val Arg Ala Lys Leu Glu Glu Gln Ala Gln Gln Ile Arg Leu Gln Ala

            260   265   270

5   Glu Ala Phe Gln Ala Arg Leu Lys Ser Trp Phe Glu Pro Leu Val Glu

            275   280   285

Asp Met Gln Arg Gln Trp Ala Gly Leu Val Glu Lys Val Gln Ala Ala

            290   295   300

Val Gly Thr Ser Ala Ala Pro Val Pro Ser Asp Asn His

10   305   310   315

<210> 60

<211> 838

15   <212> PRT

<213> Homo sapiens

<220>

<221> hypothetical 88.6 kDa protein

<222> (1)..(838)

20   <223> Accession No. as of 29 August 2003: Q96C61

<400> 60

Met Pro Ser Gly Lys Val Ala Gln Pro Thr Ile Thr Asp Asn Lys Asp

1   5   10   15

Gly Thr Val Thr Val Arg Tyr Ala Pro Ser Glu Ala Gly Leu His Glu
              20   25   30

Met Asp Ile Arg Tyr Asp Asn Met His Ile Pro Gly Ser Pro Leu Gln
              35   40   45

5 Phe Tyr Val Asp Tyr Val Asn Cys Gly His Val Thr Ala Tyr Gly Pro
              50   55   60

Gly Leu Thr His Gly Val Val Asn Lys Pro Ala Thr Phe Thr Val Asn
   65   70   75   80

Thr Lys Asp Ala Gly Glu Gly Gly Leu Ser Leu Ala Ile Glu Gly Pro
10   85   90   95

Ser Lys Ala Glu Ile Ser Cys Thr Asp Asn Gln Asp Gly Thr Cys Ser
                  100   105   110

Val Ser Tyr Leu Pro Val Leu Pro Gly Asp Tyr Ser Ile Leu Val Lys
                  115   120   125

15 Tyr Asn Glu Gln His Val Pro Gly Ser Pro Phe Thr Ala Arg Val Thr
                  130   135   140

Gly Asp Asp Ser Met Arg Met Ser His Leu Lys Val Gly Ser Ala Ala
   145   150   155   160

Asp Ile Pro Ile Asn Ile Ser Glu Thr Asp Leu Ser Leu Leu Thr Ala
20   165   170   175

Thr Val Val Pro Pro Ser Gly Arg Glu Glu Pro Cys Leu Leu Lys Arg
                  180   185   190

Leu Arg Asn Gly His Val Gly Ile Ser Phe Val Pro Lys Glu Thr Gly
                  195   200   205

```
       Glu His Leu Val His Val Lys Lys Asn Gly Gln His Val Ala Ser Ser
              210                 215                 220

       Pro Ile Pro Val Val Ile Ser Gln Ser Glu Ile Gly Asp Ala Ser Arg
       225             '     230                 235                 240

   5   Val Arg Val Ser Gly Gln Gly Leu His Glu Gly His Thr Phe Glu Pro
                           245                 250                 255

       Ala Glu Phe Ile Ile Asp Thr Arg Asp Ala Gly Tyr Gly Gly Leu Ser
                       260                 265                 270

       Leu Ser Ile Glu Gly Pro Ser Lys Val Asp Ile Asn Thr Glu Asp Leu
  10           275                 280                 285

       Glu Asp Gly Thr Cys Arg Val Thr Tyr Cys Pro Thr Glu Pro Gly Asn
                 290                 295                 300

       Tyr Ile Ile Asn Ile Lys Phe Ala Asp Gln His Val Pro Gly Ser Pro
       305                 310                 315                 320

  15   Phe Ser Val Lys Val Thr Gly Glu Gly Arg Val Lys Glu Ser Ile Thr
                       325                 330                 335

       Arg Arg Arg Arg Ala Pro Ser Val Ala Asn Val Gly Ser His Cys Asp
                 340                 345                 350

       Leu Ser Leu Lys Ile Pro Glu Ile Ser Ile Gln Asp Met Thr Ala Gln
  20           355                 360                 365

       Val Thr Ser Pro Ser Gly Lys Thr His Glu Ala Glu Ile Val Glu Gly
              370                 375                 380

       Glu Asn His Thr Tyr Cys Ile Arg Phe Val Pro Ala Glu Met Gly Thr
       385                 390                 395                 400
```

His Thr Val Ser Val Lys Tyr Lys Gly Gln His Val Pro Gly Ser Pro
                405   410   415

Phe Gln Phe Thr Val Gly Pro Leu Gly Glu Gly Gly Ala His Lys Val
                420   425   430

5   Arg Ala Gly Gly Pro Gly Leu Glu Arg Ala Glu Ala Gly Val Pro Ala
                 435   440   445

Glu Phe Ser Ile Trp Thr Arg Glu Ala Gly Ala Gly Gly Leu Ala Ile
                450   455   460

Ala Val Glu Gly Pro Ser Lys Ala Glu Ile Ser Phe Glu Asp Arg Lys
10   465   470   475   480

Asp Gly Ser Cys Gly Val Ala Tyr Val Val Gln Glu Pro Gly Asp Tyr
                485   490   495

Glu Val Ser Val Lys Phe Asn Glu Glu His Ile Pro Asp Ser Pro Phe
                500   505   510

15   Val Val Pro Val Ala Ser Pro Ser Gly Asp Ala Arg Arg Leu Thr Val
                 515   520   525

Ser Ser Leu Gln Glu Ser Gly Leu Lys Val Asn Gln Pro Ala Ser Phe
                530   535   540

Ala Val Ser Leu Asn Gly Ala Lys Gly Ala Ile Asp Ala Lys Val His
20   545   550   555   560

Ser Pro Ser Gly Ala Leu Glu Glu Cys Tyr Val Thr Glu Ile Asp Gln
                565   570   575

Asp Lys Tyr Ala Val Arg Phe Ile Pro Arg Glu Asn Gly Val Tyr Leu
                580   585   590

```
    Ile Asp Val Lys Phe Asn Gly Thr His Ile Pro Gly Ser Pro Phe Lys
            595                 600                 605

    Ile Arg Val Gly Glu Pro Gly His Gly Gly Asp Pro Gly Leu Val Ser
            610                 615                 620

 5  Ala Tyr Gly Ala Gly Leu Glu Gly Gly Val Thr Gly Asn Pro Ala Glu
    625                 630                 635                 640

    Phe Val Val Asn Thr Ser Asn Ala Gly Ala Gly Ala Leu Ser Val Thr
                    645                 650                 655

    Ile Asp Gly Pro Ser Lys Val Lys Met Asp Cys Gln Glu Cys Pro Glu
10                  660                 665                 670

    Gly Tyr Arg Val Thr Tyr Thr Pro Met Ala Pro Gly Ser Tyr Leu Ile
                    675                 680                 685

    Ser Ile Lys Tyr Gly Gly Pro Tyr His Ile Gly Gly Ser Pro Phe Lys
                690                 695                 700

15  Ala Lys Val Thr Gly Pro Arg Leu Val Ser Asn His Ser Leu His Glu
    705                 710                 715                 720

    Thr Ser Ser Val Phe Val Asp Ser Leu Thr Lys Ala Thr Cys Ala Pro
                    725                 730                 735

    Gln His Gly Ala Pro Gly Pro Gly Pro Ala Asp Ala Ser Lys Val Val
20                  740                 745                 750

    Ala Lys Gly Leu Gly Leu Ser Lys Ala Tyr Val Gly Gln Lys Ser Ser
                755                 760                 765

    Phe Thr Val Asp Cys Ser Lys Ala Gly Asn Asn Met Leu Leu Val Gly
                770                 775                 780
```

Val His Gly Pro Arg Thr Pro Cys Glu Glu Ile Leu Val Lys His Val

785   790   795   800

Gly Ser Arg Leu Tyr Ser Val Ser Tyr Leu Leu Lys Asp Lys Gly Glu

                805   810   815

5   Tyr Thr Leu Val Val Lys Trp Gly Asp Glu His Ile Pro Gly Ser Pro

                820   825   830

Tyr Arg Val Val Val Pro

                835

10

<210> 61

<211> 433

<212> PRT

<213> Homo sapiens

15 <220>

<221> human alpha enolase

<222> (1)..(433)

<223> Accession No. as of 29 August 2003: P06733

<400> 61

20

Ser Ile Leu Lys Ile His Ala Arg Glu Ile Phe Asp Ser Arg Gly Asn

1   5   10   15

Pro Thr Val Glu Val Asp Leu Phe Thr Ser Lys Gly Leu Phe Arg Ala

                20   25   30

Ala Val Pro Ser Gly Ala Ser Thr Gly Ile Tyr Glu Ala Leu Glu Leu

        35   40   45

Arg Asp Asn Asp Lys Thr Arg Tyr Met Gly Lys Gly Val Ser Lys Ala

        50   55   60

5 Val Glu His Ile Asn Lys Thr Ile Ala Pro Ala Leu Val Ser Lys Lys

        65   70   75   80

Leu Asn Val Thr Glu Gln Glu Lys Ile Asp Lys Leu Met Ile Glu Met

                85   90   95

Asp Gly Thr Glu Asn Lys Ser Lys Phe Gly Ala Asn Ala Ile Leu Gly

10   100   105   110

Val Ser Leu Ala Val Cys Lys Ala Gly Ala Val Glu Lys Gly Val Pro

            115   120   125

Leu Tyr Arg His Ile Ala Asp Leu Ala Gly Asn Ser Glu Val Ile Leu

            130   135   140

15 Pro Val Pro Ala Phe Asn Val Ile Asn Gly Gly Ser His Ala Gly Asn

    145   150   155   160

Lys Leu Ala Met Gln Glu Phe Met Ile Leu Pro Val Gly Ala Ala Asn

                165   170   175

Phe Arg Glu Ala Met Arg Ile Gly Ala Glu Val Tyr His Asn Leu Lys

20   180   185   190

Asn Val Ile Lys Glu Lys Tyr Gly Lys Asp Ala Thr Asn Val Gly Asp

            195   200   205

Glu Gly Gly Phe Ala Pro Asn Ile Leu Glu Asn Lys Glu Gly Leu Glu

            210   215   220

Leu Leu Lys Thr Ala Ile Gly Lys Ala Gly Tyr Thr Asp Lys Val Val

225   230   235   240

Ile Gly Met Asp Val Ala Ala Ser Glu Phe Phe Arg Ser Gly Lys Tyr

    245   250   255

5 Asp Leu Asp Phe Lys Ser Pro Asp Asp Pro Ser Arg Tyr Ile Ser Pro

    260   265   270

Asp Gln Leu Ala Asp Leu Tyr Lys Ser Phe Ile Lys Asp Tyr Pro Val

    275   280   285

Val Ser Ile Glu Asp Pro Phe Asp Gln Asp Asp Trp Gly Ala Trp Gln

10   290   295   300

Lys Phe Thr Ala Ser Ala Gly Ile Gln Val Val Gly Asp Asp Leu Thr

305   310   315   320

Val Thr Asn Pro Lys Arg Ile Ala Lys Ala Val Asn Glu Lys Ser Cys

    325   330   335

15 Asn Cys Leu Leu Leu Lys Val Asn Gln Ile Gly Ser Val Thr Glu Ser

    340   345   350

Leu Gln Ala Cys Lys Leu Ala Gln Ala Asn Gly Trp Gly Val Met Val

    355   360   365

Ser His Arg Ser Gly Glu Thr Glu Asp Thr Phe Ile Ala Asp Leu Val

20   370   375   380

Val Gly Leu Cys Thr Gly Gln Ile Lys Thr Gly Ala Pro Cys Arg Ser

385   390   395   400

Glu Arg Leu Ala Lys Tyr Asn Gln Leu Leu Arg Ile Glu Glu Glu Leu

    405   410   415

Gly Ser Lys Ala Lys Phe Ala Gly Arg Asn Phe Arg Asn Pro Leu Ala

                420   425   430

Lys

5

<210> 62

<211> 471

<212> PRT

10 <213> Homo sapiens

<220>

<221> tryptophanyl-tRNA synthetase

<222> (1)..(471)

<223> Accession No. as of 29 August 2003: P23381

15 <400> 62

Met Pro Asn Ser Glu Pro Ala Ser Leu Leu Glu Leu Phe Asn Ser Ile

1   5   10   15

Ala Thr Gln Gly Glu Leu Val Arg Ser Leu Lys Ala Gly Asn Ala Ser

20   20   25   30

Lys Asp Glu Ile Asp Ser Ala Val Lys Met Leu Val Ser Leu Lys Met

            35   40   45

Ser Tyr Lys Ala Ala Ala Gly Glu Asp Tyr Lys Ala Asp Cys Pro Pro

        50   55   60

Gly Asn Pro Ala Pro Thr Ser Asn His Gly Pro Asp Ala Thr Glu Ala

    65   70   75   80

Glu Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys

            85   90   95

 5 Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys Ile

            100   105   110

    Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg Pro

            115   120   125

    His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His Arg Asp Met Asn

10   130   135   140

    Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr Leu Tyr Thr

    145   150   155   160

    Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His Leu Ile Pro

                165   170   175

15 Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val Pro Leu Val

                180   185   190

    Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp Leu Thr Leu

            195   200   205

    Asp Gln Ala Tyr Ser Tyr Ala Val Glu Asn Ala Lys Asp Ile Ile Ala

20   210   215   220

    Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp Tyr

    225   230   235   240

    Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val Lys Ile Gln Lys

                245   250   255

His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly Phe Thr Asp Ser
               260   265   270

Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro Ser
               275   280   285

5 Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile Gln
               290   295   300

Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr
   305   310   315   320

Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu His
10   325   330   335

Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys Met Ser Ala
               340   345   350

Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln Ile
               355   360   365

15 Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg Asp Thr Ile
               370   375   380

Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val Asp Val Ser Phe
   385   390   395   400

Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu Glu Gln Ile
20   405   410   415

Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu Leu Lys Lys
               420   425   430

Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His Gln Ala Arg
               435   440   445

Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met Thr Pro Arg

        450   455   460

Lys Leu Ser Phe Asp Phe Gln

465   470

5

<210> 63

<211> 106

<212> PRT

10 <213> Homo sapiens

<220>

<221> Ig kappa chain C regionI

<222> (1)..(106)

<223> Accession No. as of 29 August 2003: P01834

15 <400> 63

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln

1   5   10   15

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr

20   20   25   30

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser

        35   40   45

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr

        50   55   60

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys

65   70   75   80

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro

                  85   90   95

5   Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

                  100   105

<210> 64

10 <211> 758

<212> PRT

<213> Homo sapiens

<220>

<221> Mitofilin

15 <222> (1)..(758)

<223> Accession No. as of 29 August 2003: Q16891

<400> 64

Met Leu Arg Ala Cys Gln Leu Ser Gly Val Thr Ala Ala Ala Gln Ser

20 1   5   10   15

Cys Leu Cys Gly Lys Phe Val Leu Arg Pro Leu Arg Pro Cys Arg Arg

                  20   25   30

Tyr Ser Thr Ser Gly Ser Ser Gly Leu Thr Thr Gly Lys Ile Ala Gly

            35   40   45

```
     Ala Gly Leu Leu Phe Val Gly Gly Gly Ile Gly Gly Thr Ile Leu Tyr
             50                  55                  60

     Ala Lys Trp Asp Ser His Phe Arg Glu Ser Val Glu Lys Thr Ile Pro
     65                  70                  75                  80

  5  Tyr Ser Asp Lys Leu Phe Glu Met Val Leu Gly Pro Ala Ala Tyr Asn
                         85                  90                  95

     Val Pro Leu Pro Lys Lys Ser Ile Gln Ser Gly Pro Leu Lys Ile Ser
                        100                 105                 110

     Ser Val Ser Glu Val Met Lys Glu Ser Lys Gln Pro Ala Ser Gln Leu
 10              115                 120                 125

     Gln Lys Gln Lys Gly Asp Thr Pro Ala Ser Ala Thr Ala Pro Thr Glu
                130                 135                 140

     Ala Ala Gln Ile Ile Ser Ala Ala Gly Asp Thr Leu Ser Val Pro Ala
     145                 150                 155                 160

 15  Pro Ala Val Gln Pro Glu Glu Ser Leu Lys Thr Asp His Pro Glu Ile
                        165                 170                 175

     Gly Glu Gly Lys Pro Thr Pro Ala Leu Ser Glu Glu Ala Ser Ser Ser
                180                 185                 190

     Ser Ile Arg Glu Arg Pro Pro Glu Glu Val Ala Ala Arg Leu Ala Gln
 20              195                 200                 205

     Gln Glu Lys Gln Glu Gln Val Lys Ile Glu Ser Leu Ala Lys Ser Leu
                210                 215                 220

     Glu Asp Ala Leu Arg Gln Thr Ala Ser Val Thr Leu Gln Ala Ile Ala
     225                 230                 235                 240
```

Ala Gln Asn Ala Ala Val Gln Ala Val Asn Ala His Ser Asn Ile Leu
                245   250   255

Lys Ala Ala Met Asp Asn Ser Glu Ile Ala Gly Glu Lys Lys Ser Ala
                260   265   270

5 Gln Trp Arg Thr Val Glu Gly Ala Leu Lys Glu Arg Arg Lys Ala Val
                275   280   285

Asp Glu Ala Ala Asp Ala Leu Leu Lys Ala Lys Glu Glu Leu Glu Lys
            290   295   300

Met Lys Ser Val Ile Glu Asn Ala Lys Lys Lys Glu Val Ala Gly Ala
10 305   310   315   320

Lys Pro His Ile Thr Ala Ala Glu Gly Lys Leu His Asn Met Ile Val
                325   330   335

Asp Leu Asp Asn Val Val Lys Lys Val Gln Ala Ala Gln Ser Glu Ala
                340   345   350

15 Lys Val Val Ser Gln Tyr His Glu Leu Val Val Gln Ala Arg Asp Asp
                355   360   365

Phe Lys Arg Glu Leu Asp Ser Ile Thr Pro Glu Val Leu Pro Gly Trp
                370   375   380

Lys Gly Met Ser Val Ser Asp Leu Ala Asp Lys Leu Ser Thr Asp Asp
20 385   390   395   400

Leu Asn Ser Leu Ile Ala His Ala His Arg Arg Ile Asp Gln Leu Asn
                405   410   415

Arg Glu Leu Ala Glu Gln Lys Ala Thr Glu Lys Gln His Ile Thr Leu
                420   425   430

Ala Leu Glu Lys Gln Lys Leu Glu Glu Lys Arg Ala Phe Asp Ser Ala
          435   440   445

Val Ala Lys Ala Leu Glu His His Arg Ser Glu Ile Gln Ala Glu Gln
          450   455   460

5   Asp Arg Lys Ile Glu Glu Val Arg Asp Ala Met Glu Asn Glu Met Arg
          465   470   475   480

Thr Gln Leu Arg Arg Gln Ala Ala Ala His Thr Asp His Leu Arg Asp
                  485   490   495

Val Leu Arg Val Gln Glu Gln Glu Leu Lys Ser Glu Phe Glu Gln Asn
10   500   505   510

Leu Ser Glu Lys Leu Ser Glu Gln Glu Leu Gln Phe Arg Arg Leu Ser
          515   520   525

Gln Glu Gln Val Asp Asn Phe Thr Leu Asp Ile Asn Thr Ala Tyr Ala
          530   535   540

15 Arg Leu Arg Gly Ile Glu Gln Ala Val Gln Ser His Ala Val Ala Glu
    545   550   555   560

Glu Glu Ala Arg Lys Ala His Gln Leu Trp Leu Ser Val Glu Ala Leu
          565   570   575

Lys Tyr Ser Met Lys Thr Ser Ser Ala Glu Thr Pro Thr Ile Pro Leu
20   580   585   590

Gly Ser Ala Val Glu Ala Ile Lys Ala Asn Cys Ser Asp Asn Glu Phe
          595   600   605

Thr Gln Ala Leu Thr Ala Ala Ile Pro Pro Glu Ser Leu Thr Arg Gly
          610   615   620

Val Tyr Ser Glu Glu Thr Leu Arg Ala Arg Phe Tyr Ala Val Gln Lys

625   630   635   640

Leu Ala Arg Arg Val Ala Met Ile Asp Glu Thr Arg Asn Ser Leu Tyr

                  645   650   655

5   Gln Tyr Phe Leu Ser Tyr Leu Gln Ser Leu Leu Leu Phe Pro Pro Gln

              660   665   670

Gln Leu Lys Pro Pro Pro Glu Leu Cys Pro Glu Asp Ile Asn Thr Phe

              675   680   685

Lys Leu Leu Ser Tyr Ala Ser Tyr Cys Ile Glu His Gly Asp Leu Glu

10   690   695   700

Leu Ala Ala Lys Phe Val Asn Gln Leu Lys Gly Glu Ser Arg Arg Val

705   710   715   720

Ala Gln Asp Trp Leu Lys Glu Ala Arg Met Thr Leu Glu Thr Lys Gln

                  725   730   735

15 Ile Val Glu Ile Leu Thr Ala Tyr Ala Ser Ala Val Gly Ile Gly Thr

                  740   745   750

Thr Gln Val Gln Pro Glu

              755

20

<210>   65

<211>   1410

<212>   PRT

<213>   Homo sapiens

<220>

<221>   Ribisome-binding protein 1

<222>   (1)..(1410)

<223>   Accession No. as of 29 August 2003: O75300

5   <400>   65

Met Asp Ile Tyr Asp Thr Gln Thr Leu Gly Val Val Val Phe Gly Gly

1   5   10   15

Phe Met Val Val Ser Ala Ile Gly Ile Phe Leu Val Ser Thr Phe Ser

10   20   25   30

Met Lys Glu Thr Ser Tyr Glu Glu Ala Leu Ala Asn Gln Arg Lys Glu

                35   40   45

Met Ala Lys Thr His His Gln Lys Val Glu Lys Lys Lys Lys Glu Lys

        50   55   60

15 Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn

65   70   75   80

Gly Lys Ile Pro Asp His Asp Pro Ala Pro Asn Val Thr Val Leu Leu

                85   90   95

Arg Glu Pro Val Arg Ala Pro Ala Val Ala Val Ala Pro Thr Pro Val

20   100   105   110

Gln Pro Pro Ile Ile Val Ala Pro Val Ala Thr Val Pro Ala Met Pro

                115   120   125

Gln Glu Lys Leu Ala Ser Ser Pro Lys Asp Lys Lys Lys Lys Glu Lys

        130   135   140

```
     Lys Val Ala Lys Val Glu Pro Ala Val Ser Ser Val Val Asn Ser Ile
     145                 150                 155                 160

     Gln Val Leu Thr Ser Lys Ala Ala Ile Leu Glu Thr Ala Pro Lys Glu
                         165                 170                 175

 5   Val Pro Met Val Val Val Pro Pro Val Gly Ala Lys Gly Asn Thr Pro
                     180                 185                 190

     Ala Thr Gly Thr Thr Gln Gly Lys Lys Ala Glu Gly Thr Gln Asn Gln
                 195                 200                 205

     Ser Lys Lys Ala Glu Gly Ala Pro Asn Gln Gly Arg Lys Ala Glu Gly
 10      210                 215                 220

     Thr Pro Asn Gln Gly Lys Lys Thr Glu Gly Thr Pro Asn Gln Gly Lys
     225                 230                 235                 240

     Lys Ala Glu Gly Thr Pro Asn Gln Gly Lys Lys Ala Glu Gly Thr Pro
                     245                 250                 255

 15  Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Val
                     260                 265                 270

     Asp Thr Thr Pro Asn Gln Gly Lys Lys Val Glu Gly Ala Pro Thr Gln
                 275                 280                 285

     Gly Arg Lys Ala Glu Gly Ala Gln Asn Gln Ala Lys Lys Val Glu Gly
 20      290                 295                 300

     Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys
     305                 310                 315                 320

     Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
                     325                 330                 335
```

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala

340   345   350

Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln

355   360   365

5   Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ser Glu Gly

370   375   380

Ala Gln Asn Gln Gly Lys Lys Val Glu Gly Ala Gln Asn Gln Gly Lys

385   390   395   400

Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln

10   405   410   415

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala

420   425   430

Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln

435   440   445

15 Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly

450   455   460

Ala Gln Asn Gln Gly Lys Lys Val Glu Gly Ala Gln Asn Gln Gly Lys

465   470   475   480

Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln

20   485   490   495

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Gln Lys Gly

500   505   510

Glu Gly Ala Gln Asn Gln Gly Lys Lys Thr Glu Gly Ala Gln Gly Lys

515   520   525

```
      Lys Ala Glu Arg Ser Pro Asn Gln Gly Lys Lys Gly Glu Gly Ala Pro

              530             535             540

      Ile Gln Gly Lys Lys Ala Asp Ser Val Ala Asn Gln Gly Thr Lys Val

      545             550             555             560

  5   Glu Gly Ile Thr Asn Gln Gly Lys Lys Ala Glu Gly Ser Pro Ser Glu

                  565             570             575

      Gly Lys Lys Ala Glu Gly Ser Pro Asn Gln Gly Lys Lys Ala Asp Ala

                  580             585             590

      Ala Ala Asn Gln Gly Lys Lys Thr Glu Ser Ala Ser Val Gln Gly Arg

 10           595             600             605

      Asn Thr Asp Val Ala Gln Ser Pro Glu Ala Pro Lys Gln Glu Ala Pro

              610             615             620

      Ala Lys Lys Lys Ser Gly Ser Lys Lys Lys Gly Glu Pro Gly Pro Pro

      625             630             635             640

 15   Asp Ala Asp Gly Pro Leu Tyr Leu Pro Tyr Lys Thr Leu Val Ser Thr

                  645             650             655

      Val Gly Ser Met Val Phe Asn Glu Gly Glu Ala Gln Arg Leu Ile Glu

                  660             665             670

      Ile Leu Ser Glu Lys Ala Gly Ile Ile Gln Asp Thr Trp His Lys Ala

 20           675             680             685

      Thr Gln Lys Gly Asp Pro Val Ala Ile Leu Lys Arg Gln Leu Glu Glu

              690             695             700

      Lys Glu Lys Leu Leu Ala Thr Glu Gln Glu Asp Ala Ala Val Ala Lys

      705             710             715             720
```

Ser Lys Leu Arg Glu Leu Asn Lys Glu Met Ala Ala Glu Lys Ala Lys

                725   730   735

Ala Ala Ala Gly Glu Ala Lys Val Lys Lys Gln Leu Val Ala Arg Glu

                740   745   750

5   Gln Glu Ile Thr Ala Val Gln Ala Arg Met Gln Ala Ser Tyr Arg Glu

                755   760   765

His Val Lys Glu Val Gln Gln Leu Gln Gly Lys Ile Arg Thr Leu Gln

            770   775   780

Glu Gln Leu Glu Asn Gly Pro Asn Thr Gln Leu Ala Arg Leu Gln Gln

10 785   790   795   800

Glu Asn Ser Ile Leu Arg Asp Ala Leu Asn Gln Ala Thr Ser Gln Val

                805   810   815

Glu Ser Lys Gln Asn Ala Glu Leu Ala Lys Leu Arg Gln Glu Leu Ser

                820   825   830

15 Lys Val Ser Lys Glu Leu Val Glu Lys Ser Glu Ala Val Arg Gln Asp

                835   840   845

Glu Gln Gln Arg Lys Ala Leu Glu Ala Lys Ala Ala Ala Phe Glu Lys

                850   855   860

Gln Val Leu Gln Leu Gln Ala Ser His Arg Glu Ser Glu Glu Ala Leu

20 865   870   875   880

Gln Lys Arg Leu Asp Glu Val Ser Arg Glu Leu Cys His Thr Gln Ser

                885   890   895

Ser His Ala Ser Leu Arg Ala Asp Ala Glu Lys Ala Gln Glu Gln Gln

                900   905   910

Gln Gln Met Ala Glu Leu His Ser Lys Leu Gln Ser Ser Glu Ala Glu

        915   920   925

Val Arg Ser Lys Cys Glu Glu Leu Ser Gly Leu His Gly Gln Leu Gln

        930   935   940

5   Glu Ala Arg Ala Glu Asn Ser Gln Leu Thr Glu Arg Ile Arg Ser Ile

    945   950   955   960

Glu Ala Leu Leu Glu Ala Gly Gln Ala Arg Asp Ala Gln Asp Val Gln

            965   970   975

Ala Ser Gln Ala Glu Ala Asp Gln Gln Gln Thr Arg Leu Lys Glu Leu

10   980   985   990

Glu Ser Gln Val Ser Gly Leu Glu Lys Glu Ala Ile Glu Leu Arg Glu

        995   1000   1005

Ala Val Glu Gln Gln Lys Val Lys Asn Asn Asp Leu Arg Glu Lys

        1010   1015   1020

15 Asn Trp Lys Ala Met Glu Ala Leu Ala Thr Ala Glu Gln Ala Cys

        1025   1030   1035

Lys Glu Lys Leu Leu Ser Leu Thr Gln Ala Lys Glu Glu Ser Glu

        1040   1045   1050

Lys Gln Leu Cys Leu Ile Glu Ala Gln Thr Met Glu Ala Leu Leu

20   1055   1060   1065

Ala Leu Leu Pro Glu Leu Ser Val Leu Ala Gln Gln Asn Tyr Thr

        1070   1075   1080

Glu Trp Leu Gln Asp Leu Lys Glu Lys Gly Pro Thr Leu Leu Lys

        1085   1090   1095

```
      His Pro  Pro Ala Pro Ala Glu  Pro Ser Ser Asp Leu  Ala Ser Lys
          1100             1105             1110

      Leu Arg  Glu Ala Glu Glu Thr  Gln Ser Thr Leu Gln  Ala Glu Cys
          1115             1120             1125

 5    Asp Gln  Tyr Arg Ser Ile Leu  Ala Glu Thr Glu Gly  Met Leu Arg
          1130             1135             1140

      Asp Leu  Gln Lys Ser Val Glu  Glu Glu Glu Gln Val  Trp Arg Ala
          1145             1150             1155

      Lys Val  Gly Ala Ala Glu Glu  Glu Leu Gln Lys Ser  Arg Val Thr
10        1160             1165             1170

      Val Lys  His Leu Glu Glu Ile  Val Glu Lys Leu Lys  Gly Glu Leu
          1175             1180             1185

      Glu Ser  Ser Asp Gln Val Arg  Glu His Thr Ser His  Leu Glu Ala
          1190             1195             1200

15    Glu Leu  Glu Lys His Met Ala  Ala Ala Ser Ala Glu  Cys Gln Asn
          1205             1210             1215

      Tyr Ala  Lys Glu Val Ala Gly  Leu Arg Gln Leu Leu  Leu Glu Ser
          1220             1225             1230

      Gln Ser  Gln Leu Asp Ala Ala  Lys Ser Glu Ala Gln  Lys Gln Ser
20        1235             1240             1245

      Asp Glu  Leu Ala Leu Val Arg  Gln Gln Leu Ser Glu  Met Lys Ser
          1250             1255             1260

      His Val  Glu Asp Gly Asp Ile  Ala Gly Ala Pro Ala  Ser Ser Pro
          1265             1270             1275
```

Glu Ala   Pro Pro Ala Glu Gln   Asp Pro Val Gln Leu   Lys Thr Gln

      1280   1285   1290

Leu Glu   Trp Thr Glu Ala Ile   Leu Glu Asp Glu Gln   Thr Gln Arg

      1295   1300   1305

5   Gln Lys   Leu Thr Ala Glu Phe   Glu Glu Ala Gln Thr   Ser Ala Cys

      1310   1315   1320

Arg Leu   Gln Glu Glu Leu Glu   Lys Leu Arg Thr Ala   Gly Pro Leu

      1325   1330   1335

Glu Ser   Ser Glu Thr Glu Glu   Ala Ser Gln Leu Lys   Glu Arg Leu

10   1340   1345   1350

Glu Lys   Glu Lys Lys Leu Thr   Ser Asp Leu Gly Arg   Ala Ala Thr

      1355   1360   1365

Arg Leu   Gln Glu Leu Leu Lys   Thr Thr Gln Glu Gln   Leu Ala Arg

      1370   1375   1380

15   Glu Lys   Asp Thr Val Lys Lys   Leu Gln Glu Gln Leu   Glu Lys Ala

      1385   1390   1395

Glu Asp   Gly Ser Ser Ser Lys   Glu Gly Thr Ser Val

      1400   1405   1410

20

<210>   66

<211>   453

<212>   PRT

<213>   Homo sapiens

<220>

<221> Fibrinogen gamma chain precursor

<222> (1)..(453)

<223> Accession No. as of 29 August 2003: P02679

5   <400> 66


```
     Met Ser Trp Ser Leu His Pro Arg Asn Leu Ile Leu Tyr Phe Tyr Ala

     1               5                   10                  15

     Leu Leu Phe Leu Ser Ser Thr Cys Val Ala Tyr Val Ala Thr Arg Asp

10               20                  25                  30

     Asn Cys Cys Ile Leu Asp Glu Arg Phe Gly Ser Tyr Cys Pro Thr Thr

                 35                  40                  45

     Cys Gly Ile Ala Asp Phe Leu Ser Thr Tyr Gln Thr Lys Val Asp Lys

                 50                  55                  60

15   Asp Leu Gln Ser Leu Glu Asp Ile Leu His Gln Val Glu Asn Lys Thr

     65                  70                  75                  80

     Ser Glu Val Lys Gln Leu Ile Lys Ala Ile Gln Leu Thr Tyr Asn Pro

                     85                  90                  95

     Asp Glu Ser Ser Lys Pro Asn Met Ile Asp Ala Ala Thr Leu Lys Ser

20               100                 105                 110

     Arg Lys Met Leu Glu Glu Ile Met Lys Tyr Glu Ala Ser Ile Leu Thr

                 115                 120                 125

     His Asp Ser Ser Ile Arg Tyr Leu Gln Glu Ile Tyr Asn Ser Asn Asn

                 130                 135                 140
```

Gln Lys Ile Val Asn Leu Lys Glu Lys Val Ala Gln Leu Glu Ala Gln

145   150   155   160

Cys Gln Glu Pro Cys Lys Asp Thr Val Gln Ile His Asp Ile Thr Gly

                165   170   175

5 Lys Asp Cys Gln Asp Ile Ala Asn Lys Gly Ala Lys Gln Ser Gly Leu

              180   185   190

Tyr Phe Ile Lys Pro Leu Lys Ala Asn Gln Gln Phe Leu Val Tyr Cys

        195   200   205

Glu Ile Asp Gly Ser Gly Asn Gly Trp Thr Val Phe Gln Lys Arg Leu

10   210   215   220

Asp Gly Ser Val Asp Phe Lys Lys Asn Trp Ile Gln Tyr Lys Glu Gly

225   230   235   240

Phe Gly His Leu Ser Pro Thr Gly Thr Thr Glu Phe Trp Leu Gly Asn

              245   250   255

15 Glu Lys Ile His Leu Ile Ser Thr Gln Ser Ala Ile Pro Tyr Ala Leu

              260   265   270

Arg Val Glu Leu Glu Asp Trp Asn Gly Arg Thr Ser Thr Ala Asp Tyr

        275   280   285

Ala Met Phe Lys Val Gly Pro Glu Ala Asp Lys Tyr Arg Leu Thr Tyr

20   290   295   300

Ala Tyr Phe Ala Gly Gly Asp Ala Gly Asp Ala Phe Asp Gly Phe Asp

305   310   315   320

Phe Gly Asp Asp Pro Ser Asp Lys Phe Phe Thr Ser His Asn Gly Met

              325   330   335

Gln Phe Ser Thr Trp Asp Asn Asp Asn Asp Lys Phe Glu Gly Asn Cys

            340   345   350

Ala Glu Gln Asp Gly Ser Gly Trp Trp Met Asn Lys Cys His Ala Gly

        355   360   365

5   His Leu Asn Gly Val Tyr Tyr Gln Gly Gly Thr Tyr Ser Lys Ala Ser

        370   375   380

Thr Pro Asn Gly Tyr Asp Asn Gly Ile Ile Trp Ala Thr Trp Lys Thr

385   390   395   400

Arg Trp Tyr Ser Met Lys Lys Thr Thr Met Lys Ile Ile Pro Phe Asn

10   405   410   415

Arg Leu Thr Ile Gly Glu Gly Gln Gln His His Leu Gly Gly Ala Lys

            420   425   430

Gln Val Arg Pro Glu His Pro Ala Glu Thr Glu Tyr Asp Ser Leu Tyr

        435   440   445

15 Pro Glu Asp Asp Leu

        450

    <210>   67

20 <211>   622

    <212>   PRT

    <213>   Homo sapiens

    <220>

    <221>   Prothrombin percursor

<222>   (1)..(622)

<223>   Accession No. as of 29 August 2003: P00734

<400>   67

5   Met Ala His Val Arg Gly Leu Gln Leu Pro Gly Cys Leu Ala Leu Ala

     1   5   10   15

     Ala Leu Cys Ser Leu Val His Ser Gln His Val Phe Leu Ala Pro Gln

                      20   25   30

     Gln Ala Arg Ser Leu Leu Gln Arg Val Arg Arg Ala Asn Thr Phe Leu

10   35   40   45

     Glu Glu Val Arg Lys Gly Asn Leu Glu Arg Glu Cys Val Glu Glu Thr

              50   55   60

     Cys Ser Tyr Glu Glu Ala Phe Glu Ala Leu Glu Ser Ser Thr Ala Thr

              65   70   75   80

15   Asp Val Phe Trp Ala Lys Tyr Thr Ala Cys Glu Thr Ala Arg Thr Pro

                      85   90   95

     Arg Asp Lys Leu Ala Ala Cys Leu Glu Gly Asn Cys Ala Glu Gly Leu

                      100   105   110

     Gly Thr Asn Tyr Arg Gly His Val Asn Ile Thr Arg Ser Gly Ile Glu

20   115   120   125

     Cys Gln Leu Trp Arg Ser Arg Tyr Pro His Lys Pro Glu Ile Asn Ser

              130   135   140

     Thr Thr His Pro Gly Ala Asp Leu Gln Glu Asn Phe Cys Arg Asn Pro

     145   150   155   160

```
     Asp Ser Ser Thr Thr Gly Pro Trp Cys Tyr Thr Thr Asp Pro Thr Val
                     165                 170                 175

     Arg Arg Gln Glu Cys Ser Ile Pro Val Cys Gly Gln Asp Gln Val Thr
                     180                 185                 190

  5  Val Ala Met Thr Pro Arg Ser Glu Gly Ser Ser Val Asn Leu Ser Pro
                     195                 200                 205

     Pro Leu Glu Gln Cys Val Pro Asp Arg Gly Gln Gln Tyr Gln Gly Arg
                     210                 215                 220

 10  Leu Ala Val Thr Thr His Gly Leu Pro Cys Leu Ala Trp Ala Ser Ala
     225                 230                 235                 240

     Gln Ala Lys Ala Leu Ser Lys His Gln Asp Phe Asn Ser Ala Val Gln
                     245                 250                 255

     Leu Val Glu Asn Phe Cys Arg Asn Pro Asp Gly Asp Glu Glu Gly Val
                     260                 265                 270

 15  Trp Cys Tyr Val Ala Gly Lys Pro Gly Asp Phe Gly Tyr Cys Asp Leu
                     275                 280                 285

     Asn Tyr Cys Glu Glu Ala Val Glu Glu Glu Thr Gly Asp Gly Leu Asp
                     290                 295                 300

     Glu Asp Ser Asp Arg Ala Ile Glu Gly Arg Thr Ala Thr Ser Glu Tyr
 20  305                 310                 315                 320

     Gln Thr Phe Phe Asn Pro Arg Thr Phe Gly Ser Gly Glu Ala Asp Cys
                     325                 330                 335

     Gly Leu Arg Pro Leu Phe Glu Lys Lys Ser Leu Glu Asp Lys Thr Glu
                     340                 345                 350
```

Arg Glu Leu Leu Glu Ser Tyr Ile Asp Gly Arg Ile Val Glu Gly Ser

     355   360   365

Asp Ala Glu Ile Gly Met Ser Pro Trp Gln Val Met Leu Phe Arg Lys

     370   375   380

5 Ser Pro Gln Glu Leu Leu Cys Gly Ala Ser Leu Ile Ser Asp Arg Trp

     385   390   395   400

Val Leu Thr Ala Ala His Cys Leu Leu Tyr Pro Pro Trp Asp Lys Asn

            405   410   415

Phe Thr Glu Asn Asp Leu Leu Val Arg Ile Gly Lys His Ser Arg Thr

10   420   425   430

Arg Tyr Glu Arg Asn Ile Glu Lys Ile Ser Met Leu Glu Lys Ile Tyr

     435   440   445

Ile His Pro Arg Tyr Asn Trp Arg Glu Asn Leu Asp Arg Asp Ile Ala

     450   455   460

15 Leu Met Lys Leu Lys Lys Pro Val Ala Phe Ser Asp Tyr Ile His Pro

465   470   475   480

Val Cys Leu Pro Asp Arg Glu Thr Ala Ala Ser Leu Leu Gln Ala Gly

            485   490   495

Tyr Lys Gly Arg Val Thr Gly Trp Gly Asn Leu Lys Glu Thr Trp Thr

20   500   505   510

Ala Asn Val Gly Lys Gly Gln Pro Ser Val Leu Gln Val Val Asn Leu

     515   520   525

Pro Ile Val Glu Arg Pro Val Cys Lys Asp Ser Thr Arg Ile Arg Ile

     530   535   540

Thr Asp Asn Met Phe Cys Ala Gly Tyr Lys Pro Asp Glu Gly Lys Arg

545   550   555   560

Gly Asp Ala Cys Glu Gly Asp Ser Gly Gly Pro Phe Val Met Lys Ser

565   570   575

5   Pro Phe Asn Asn Arg Trp Tyr Gln Met Gly Ile Val Ser Trp Gly Glu

580   585   590

Gly Cys Asp Arg Asp Gly Lys Tyr Gly Phe Tyr Thr His Val Phe Arg

595   600   605

Leu Lys Lys Trp Ile Gln Lys Val Ile Asp Gln Phe Gly Glu

10   610   615   620

<210> 68

<211> 530

15 <212> PRT

<213> Homo sapiens

<220>

<221> Pyruvate kinase

<222> (1)..(530)

20 <223> Accession No. as of 29 August 2003: P14618

<400> 68

Ser Lys Pro His Ser Glu Ala Gly Thr Ala Phe Ile Gln Thr Gln Gln

1   5   10   15

```
     Leu His Ala Ala Met Ala Asp Thr Phe Leu Glu His Met Cys Arg Leu
              20                  25                  30

     Asp Ile Asp Ser Pro Pro Ile Thr Ala Arg Asn Thr Gly Ile Ile Cys
              35                  40                  45

  5  Thr Ile Gly Pro Ala Ser Arg Ser Val Glu Thr Leu Lys Glu Met Ile
              50                  55                  60

     Lys Ser Gly Met Asn Val Ala Arg Leu Asn Phe Ser His Gly Thr His
         65                  70                  75                  80

     Glu Tyr His Ala Glu Thr Ile Lys Asn Val Arg Thr Ala Thr Glu Ser
 10                  85                  90                  95

     Phe Ala Ser Asp Pro Ile Leu Tyr Arg Pro Val Ala Val Ala Leu Asp
                  100                 105                 110

     Thr Lys Gly Pro Glu Ile Arg Thr Gly Leu Ile Lys Gly Ser Gly Thr
                  115                 120                 125

 15  Ala Glu Val Glu Leu Lys Lys Gly Ala Thr Leu Lys Ile Thr Leu Asp
                  130                 135                 140

     Asn Ala Tyr Met Glu Lys Cys Asp Glu Asn Ile Leu Trp Leu Asp Tyr
         145                 150                 155                 160

     Lys Asn Ile Cys Lys Val Val Glu Val Gly Ser Lys Ile Tyr Val Asp
 20                  165                 170                 175

     Asp Gly Leu Ile Ser Leu Gln Val Lys Gln Lys Gly Ala Asp Phe Leu
                  180                 185                 190

     Val Thr Glu Val Glu Asn Gly Gly Ser Leu Gly Ser Lys Lys Gly Val
                  195                 200                 205
```

```
    Asn Leu Pro Gly Ala Ala Val Asp Leu Pro Ala Val Ser Glu Lys Asp
            210             215             220

    Ile Gln Asp Leu Lys Phe Gly Val Glu Gln Asp Val Asp Met Val Phe
    225             230             235             240

  5 Ala Ser Phe Ile Arg Lys Ala Ser Asp Val His Glu Val Arg Lys Val
                    245             250             255

    Leu Gly Glu Lys Gly Lys Asn Ile Lys Ile Ile Ser Lys Ile Glu Asn
            260             265             270

    His Glu Gly Val Arg Arg Phe Asp Glu Ile Leu Glu Ala Ser Asp Gly
 10         275             280             285

    Ile Met Val Ala Arg Gly Asp Leu Gly Ile Glu Ile Pro Ala Glu Lys
            290             295             300

    Val Phe Leu Ala Gln Lys Met Met Ile Gly Arg Cys Asn Arg Ala Gly
    305             310             315             320

 15 Lys Pro Val Ile Cys Ala Thr Gln Met Leu Glu Ser Met Ile Lys Lys
                    325             330             335

    Pro Arg Pro Thr Arg Ala Glu Gly Ser Asp Val Ala Asn Ala Val Leu
            340             345             350

    Asp Gly Ala Asp Cys Ile Met Leu Ser Gly Glu Thr Ala Lys Gly Asp
 20         355             360             365

    Tyr Pro Leu Glu Ala Val Arg Met Gln His Leu Ile Ala Arg Glu Ala
            370             375             380

    Glu Ala Ala Ile Tyr His Leu Gln Leu Phe Glu Glu Leu Arg Arg Leu
    385             390             395             400
```

```
      Ala Pro Ile Thr Ser Asp Pro Thr Glu Ala Thr Ala Val Gly Ala Val
                      405                 410                 415

      Glu Ala Ser Phe Lys Cys Cys Ser Gly Ala Ile Ile Val Leu Thr Lys
                      420                 425                 430

   5  Ser Gly Arg Ser Ala His Gln Val Ala Arg Tyr Arg Pro Arg Ala Pro
                      435                 440                 445

      Ile Ile Ala Val Thr Arg Asn Pro Gln Thr Ala Arg Gln Ala His Leu
                  450                 455                 460

      Tyr Arg Gly Ile Phe Pro Val Leu Cys Lys Asp Pro Val Gln Glu Ala
  10  465                 470                 475                 480

      Trp Ala Glu Asp Val Asp Leu Arg Val Asn Phe Ala Met Asn Val Gly
                      485                 490                 495

      Lys Ala Arg Gly Phe Phe Lys Lys Gly Asp Val Val Ile Val Leu Thr
                  500                 505                 510

  15  Gly Trp Arg Pro Gly Ser Gly Phe Thr Asn Thr Met Arg Val Val Pro
                  515                 520                 525

      Val Pro

                  530



  20


      <210>   69

      <211>   328

      <212>   PRT

      <213>   Homo sapiens
```

<220>

<221>   Reticulocalbin 3 precursor

<222>   (1)..(328)

<223>   Accession No. as of 29 August 2003: Q96D15

5   <400>   69

Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

1   5   10   15

Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly

10   20   25   30

Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala

         35   40   45

His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val

         50   55   60

15   Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu

65   70   75   80

Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp

              85   90   95

Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg

20   100   105   110

His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp

         115   120   125

Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly

         130   135   140

His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr
145   150   155   160

Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp
                     165   170   175

5   Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu
                     180   185   190

His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr
                195   200   205

Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu
10   210   215   220

Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala
225   230   235   240

Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn
                     245   250   255

15 Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro
                     260   265   270

Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu
                275   280   285

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
20   290   295   300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
305   310   315   320

Leu Thr Arg His His Asp Glu Leu
                325

<210> 70

<211> 469

5 <212> PRT

<213> Homo sapiens

<220>

<221> Desmin

<222> (1)..(469)

10 <223> Accession No. as of 29 August 2003: P17661

<400> 70

Ser Gln Ala Tyr Ser Ser Ser Gln Arg Val Ser Ser Tyr Arg Arg Thr

1   5   10   15

15 Phe Gly Gly Ala Pro Gly Phe Pro Leu Gly Ser Pro Leu Ser Ser Pro

                20   25   30

Val Phe Pro Arg Ala Gly Phe Gly Ser Lys Gly Ser Ser Ser Ser Val

        35   40   45

Thr Ser Arg Val Tyr Gln Val Ser Arg Thr Ser Gly Gly Ala Gly Gly

20   50   55   60

Leu Gly Ser Leu Arg Ala Ser Arg Leu Gly Thr Thr Arg Thr Pro Ser

65   70   75   80

Ser Tyr Gly Ala Gly Glu Leu Leu Asp Phe Ser Leu Ala Asp Ala Val

                85   90   95

Asn Gln Glu Phe Leu Thr Thr Arg Thr Asn Glu Lys Val Glu Leu Gln

        100   105   110

Glu Leu Asn Asp Arg Phe Ala Asn Tyr Ile Glu Lys Val Arg Phe Leu

        115   120   125

5 Glu Gln Gln Asn Ala Ala Leu Ala Ala Glu Val Asn Arg Leu Lys Gly

        130   135   140

Arg Glu Pro Thr Arg Val Ala Glu Leu Tyr Glu Glu Glu Leu Arg Glu

        145   150   155   160

Leu Arg Arg Gln Val Glu Val Leu Thr Asn Gln Arg Ala Arg Val Asp

10   165   170   175

Val Glu Arg Asp Asn Leu Leu Asp Asp Leu Gln Arg Leu Lys Ala Lys

            180   185   190

Leu Gln Glu Glu Ile Gln Leu Lys Glu Glu Ala Glu Asn Asn Leu Ala

         195   200   205

15 Ala Phe Arg Ala Asp Val Asp Ala Ala Thr Leu Ala Arg Ile Asp Leu

        210   215   220

Glu Arg Arg Ile Glu Ser Leu Asn Glu Glu Ile Ala Phe Leu Lys Lys

225   230   235   240

Val His Glu Glu Glu Ile Arg Glu Leu Gln Ala Gln Leu Gln Glu Gln

20   245   250   255

Gln Val Gln Val Glu Met Asp Met Ser Lys Pro Asp Leu Thr Ala Ala

        260   265   270

Leu Arg Asp Ile Arg Ala Gln Tyr Glu Thr Ile Ala Ala Lys Asn Ile

        275   280   285

Ser Glu Ala Glu Glu Trp Tyr Lys Ser Lys Val Ser Asp Leu Thr Gln

        290   295   300

Ala Ala Asn Lys Asn Asn Asp Ala Leu Arg Gln Ala Lys Gln Glu Met

305   310   315   320

5 Met Glu Tyr Arg His Gln Ile Gln Ser Tyr Thr Cys Glu Ile Asp Ala

                325   330   335

Leu Lys Gly Thr Asn Asp Ser Leu Met Arg Gln Met Arg Glu Leu Glu

            340   345   350

Asp Arg Phe Ala Ser Glu Ala Ser Gly Tyr Gln Asp Asn Ile Ala Arg

10   355   360   365

Leu Glu Glu Glu Ile Arg His Leu Lys Asp Glu Met Ala Arg His Leu

            370   375   380

Arg Glu Tyr Gln Asp Leu Leu Asn Val Lys Met Ala Leu Asp Val Glu

385   390   395   400

15 Ile Ala Thr Tyr Arg Lys Leu Leu Glu Gly Glu Glu Ser Arg Ile Asn

                405   410   415

Leu Pro Ile Gln Thr Tyr Ser Ala Leu Asn Phe Arg Glu Thr Ser Pro

            420   425   430

Glu Gln Arg Gly Ser Glu Val His Thr Lys Lys Thr Val Met Ile Lys

20   435   440   445

Thr Ile Glu Thr Arg Asp Gly Glu Val Val Ser Glu Ala Thr Gln Gln

            450   455   460

Gln His Glu Val Leu

465

<210> 71

<211> 417

5 <212> PRT

<213> Homo sapiens

<220>

<221> Carboxypeptidase B precursor

<222> (1)..(417)

10 <223> Accession No. as of 29 August 2003: P15086

<400> 71


```
    Met Leu Ala Leu Leu Val Leu Val Thr Val Ala Leu Ala Ser Ala His

    1               5                   10                  15

15  His Gly Gly Glu His Phe Glu Gly Glu Lys Val Phe Arg Val Asn Val

                    20                  25                  30

    Glu Asp Glu Asn His Ile Asn Ile Ile Arg Glu Leu Ala Ser Thr Thr

                35                  40                  45

    Gln Ile Asp Phe Trp Lys Pro Asp Ser Val Thr Gln Ile Lys Pro His

20      50                  55                  60

    Ser Thr Val Asp Phe Arg Val Lys Ala Glu Asp Thr Val Thr Val Glu

        65                  70                  75                  80

    Asn Val Leu Lys Gln Asn Glu Leu Gln Tyr Lys Val Leu Ile Ser Asn

                    85                  90                  95
```

Leu Arg Asn Val Val Glu Ala Gln Phe Asp Ser Arg Val Arg Ala Thr
              100   105   110

Gly His Ser Tyr Glu Lys Tyr Asn Lys Trp Glu Thr Ile Glu Ala Trp
              115   120   125

5   Thr Gln Gln Val Ala Thr Glu Asn Pro Ala Leu Ile Ser Arg Ser Val
              130   135   140

Ile Gly Thr Thr Phe Glu Gly Arg Ala Ile Tyr Leu Leu Lys Val Gly
    145   150   155   160

Lys Ala Gly Gln Asn Lys Pro Ala Ile Phe Met Asp Cys Gly Phe His
10   165   170   175

Ala Arg Glu Trp Ile Ser Pro Ala Phe Cys Gln Trp Phe Val Arg Glu
                  180   185   190

Ala Val Arg Thr Tyr Gly Arg Glu Ile Gln Val Thr Glu Leu Leu Asp
                  195   200   205

15 Lys Leu Asp Phe Tyr Val Leu Pro Val Leu Asn Ile Asp Gly Tyr Ile
              210   215   220

Tyr Thr Trp Thr Lys Ser Arg Phe Trp Arg Lys Thr Arg Ser Thr His
    225   230   235   240

Thr Gly Ser Ser Cys Ile Gly Thr Asp Pro Asn Arg Asn Phe Asp Ala
20   245   250   255

Gly Trp Cys Glu Ile Gly Ala Ser Arg Asn Pro Cys Asp Glu Thr Tyr
                  260   265   270

Cys Gly Pro Ala Ala Glu Ser Glu Lys Glu Thr Lys Ala Leu Ala Asp
                  275   280   285

Phe Ile Arg Asn Lys Leu Ser Ser Ile Lys Ala Tyr Leu Thr Ile His

290   295   300

Ser Tyr Ser Gln Met Met Ile Tyr Pro Tyr Ser Tyr Ala Tyr Lys Leu

305   310   315   320

5   Gly Glu Asn Asn Ala Glu Leu Asn Ala Leu Ala Lys Ala Thr Val Lys

325   330   335

Glu Leu Ala Ser Leu His Gly Thr Lys Tyr Thr Tyr Gly Pro Gly Ala

340   345   350

Thr Thr Ile Tyr Pro Ala Ala Gly Gly Ser Asp Asp Trp Ala Tyr Asp

10   355   360   365

Gln Gly Ile Arg Tyr Ser Phe Thr Phe Glu Leu Arg Asp Thr Gly Arg

370   375   380

Tyr Gly Phe Leu Leu Pro Glu Ser Gln Ile Arg Ala Thr Cys Glu Glu

385   390   395   400

15 Thr Phe Leu Ala Ile Lys Tyr Val Ala Ser Tyr Val Leu Glu His Leu

405   410   415

Tyr

20

<210> 72

<211> 419

<212> PRT

<213> Homo sapiens

<220>

<221>   Carboxypeptidase A1 precursor

<222>   (1)..(419)

<223>   Accession No. as of 29 August 2003: P15085

5   <400>   72

Met Arg Gly Leu Leu Val Leu Ser Val Leu Leu Gly Ala Val Phe Gly

1   5   10   15

Lys Glu Asp Phe Val Gly His Gln Val Leu Arg Ile Ser Val Ala Asp

10   20   25   30

Glu Ala Gln Val Gln Lys Val Lys Glu Leu Glu Asp Leu Glu His Leu

                35   40   45

Gln Leu Asp Phe Trp Arg Gly Pro Ala His Pro Gly Ser Pro Ile Asp

                50   55   60

15 Val Arg Val Pro Phe Pro Ser Ile Gln Ala Val Lys Ile Phe Leu Glu

    65   70   75   80

Ser His Gly Ile Ser Tyr Glu Thr Met Ile Glu Asp Val Gln Ser Leu

                85   90   95

Leu Asp Glu Glu Gln Glu Gln Met Phe Ala Phe Arg Ser Arg Ala Arg

20   100   105   110

Ser Thr Asp Thr Phe Asn Tyr Ala Thr Tyr His Thr Leu Glu Glu Ile

                115   120   125

Tyr Asp Phe Leu Asp Leu Leu Val Ala Glu Asn Pro His Leu Val Ser

                130   135   140

Lys Ile Gln Ile Gly Asn Thr Tyr Glu Gly Arg Pro Ile Tyr Val Leu

145　　　　　　　150　　　　　　　155　　　　　　　160

Lys Phe Ser Thr Gly Gly Ser Lys Arg Pro Ala Ile Trp Ile Asp Thr

　　　　　　165　　　　　　　170　　　　　　　175

5　Gly Ile His Ser Arg Glu Trp Val Thr Gln Ala Ser Gly Val Trp Phe

　　　　　　180　　　　　　　185　　　　　　　190

Ala Lys Lys Ile Thr Gln Asp Tyr Gly Gln Asp Ala Ala Phe Thr Ala

　　　　195　　　　　　　200　　　　　　　205

Ile Leu Asp Thr Leu Asp Ile Phe Leu Glu Ile Val Thr Asn Pro Asp

10　　210　　　　　　　215　　　　　　　220

Gly Phe Ala Phe Thr His Ser Thr Asn Arg Met Trp Arg Lys Thr Arg

225　　　　　　　230　　　　　　　235　　　　　　　240

Ser His Thr Ala Gly Ser Leu Cys Ile Gly Val Asp Pro Asn Arg Asn

　　　　　　245　　　　　　　250　　　　　　　255

15　Trp Asp Ala Gly Phe Gly Leu Ser Gly Ala Ser Ser Asn Pro Cys Ser

　　　　　　260　　　　　　　265　　　　　　　270

Glu Thr Tyr His Gly Lys Phe Ala Asn Ser Glu Val Glu Val Lys Ser

　　　　275　　　　　　　280　　　　　　　285

Ile Val Asp Phe Val Lys Asp His Gly Asn Ile Lys Ala Phe Ile Ser

20　　290　　　　　　　295　　　　　　　300

Ile His Ser Tyr Ser Gln Leu Leu Met Tyr Pro Tyr Gly Tyr Lys Thr

305　　　　　　　310　　　　　　　315　　　　　　　320

Glu Pro Val Pro Asp Gln Asp Glu Leu Asp Gln Leu Ser Lys Ala Ala

　　　　　　325　　　　　　　330　　　　　　　335

Val Thr Ala Leu Ala Ser Leu Tyr Gly Thr Lys Phe Asn Tyr Gly Ser
              340   345   350

Ile Ile Lys Ala Ile Tyr Gln Ala Ser Gly Ser Thr Ile Asp Trp Thr
              355   360   365

5   Tyr Ser Gln Gly Ile Lys Tyr Ser Phe Thr Phe Glu Leu Arg Asp Thr
              370   375   380

Gly Arg Tyr Gly Phe Leu Leu Pro Ala Ser Gln Ile Ile Pro Thr Ala

385   390   395   400

Lys Glu Thr Trp Leu Ala Leu Leu Thr Ile Met Glu His Thr Leu Asn

10   405   410   415

His Pro Tyr

15 <210> 73

    <211> 418

    <212> PRT

    <213> Homo sapiens

    <220>

20 <221> Colligin 2

    <222> (1)..(418)

    <223> Accession No. as of 29 August 2003: P50454

    <400> 73

```
      Met Arg Ser Leu Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala
      1               5                   10                  15

      Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Pro Gly Thr
                      20                  25              30

   5  Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Ser Ala
                      35                  40                  45

      Gly Leu Ala Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val
                  50                  55                  60

      Glu Asn Ile Leu Val Ser Pro Val Val Val Ala Ser Ser Leu Gly Leu
  10  65                  70                  75                  80

      Val Ser Leu Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val
                      85                  90                  95

      Leu Ser Ala Glu Gln Leu Arg Asp Glu Glu Val His Ala Gly Leu Gly
                      100                 105                 110

  15  Glu Leu Leu Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp
                      115                 120                 125

      Lys Leu Gly Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp
                  130                 135                 140

      Asp Phe Val Arg Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys
  20  145                 150                 155                 160

      Ile Asn Phe Arg Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp
                      165                 170                 175

      Ala Ala Gln Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val
                      180                 185                 190
```

```
     Glu Arg Thr Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro
              195                 200                 205

     His Trp Asp Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe
              210                 215                 220

 5   Met Val Thr Arg Ser Tyr Thr Val Gly Val Met Met Met His Arg Thr
     225                 230                 235                 240

     Gly Leu Tyr Asn Tyr Tyr Asp Asp Glu Lys Glu Lys Leu Gln Ile Val
                      245                 250                 255

     Glu Met Pro Leu Ala His Lys Leu Ser Ser Leu Ile Ile Leu Met Pro
10                   260                 265                 270

     His His Val Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu
              275                 280                 285

     Gln Leu Lys Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile
              290                 295                 300

15   Ser Leu Pro Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His
     305                 310                 315                 320

     Leu Ala Gly Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp
                      325                 330                 335

     Leu Ser Arg Met Ser Gly Lys Lys Asp Leu Tyr Leu Ala Ser Val Phe
20                   340                 345                 350

     His Ala Thr Ala Phe Glu Leu Asp Thr Asp Gly Asn Pro Phe Asp Gln
              355                 360                 365

     Asp Ile Tyr Gly Arg Glu Glu Leu Arg Ser Pro Lys Leu Phe Tyr Ala
              370                 375                 380
```

Asp His Pro Phe Ile Phe Leu Val Arg Asp Thr Gln Ser Gly Ser Leu

    385   390   395   400

Leu Phe Ile Gly Arg Leu Val Arg Pro Lys Gly Asp Lys Met Arg Asp

                    405   410   415

5   Glu Leu

    <210>   74

10 <211>   263

    <212>   PRT

    <213>   Homo sapiens

    <220>

    <221>   Chymotrypsinogen B precursor

15 <222>   (1)..(263)

    <223>   Accession No. as of 29 August 2003: P17538

    <400>   74

Met Ala Phe Leu Trp Leu Leu Ser Cys Trp Ala Leu Leu Gly Thr Thr

20 1   5   10   15

Phe Gly Cys Gly Val Pro Ala Ile His Pro Val Leu Ser Gly Leu Ser

                20   25   30

Arg Ile Val Asn Gly Glu Asp Ala Val Pro Gly Ser Trp Pro Trp Gln

            35   40   45

```
      Val Ser Leu Gln Asp Lys Thr Gly Phe His Phe Cys Gly Gly Ser Leu
              50                  55                  60

      Ile Ser Glu Asp Trp Val Val Thr Ala Ala His Cys Gly Val Arg Thr
      65                  70                  75                  80

   5  Ser Asp Val Val Val Ala Gly Glu Phe Asp Gln Gly Ser Asp Glu Glu
                      85                  90                  95

      Asn Ile Gln Val Leu Lys Ile Ala Lys Val Phe Lys Asn Pro Lys Phe
                     100                 105                 110

      Ser Ile Leu Thr Val Asn Asn Asp Ile Thr Leu Leu Lys Leu Ala Thr
  10         115                 120                 125

      Pro Ala Arg Phe Ser Gln Thr Val Ser Ala Val Cys Leu Pro Ser Ala
                 130                 135                 140

      Asp Asp Asp Phe Pro Ala Gly Thr Leu Cys Ala Thr Thr Gly Trp Gly
      145                 150                 155                 160

  15  Lys Thr Lys Tyr Asn Ala Asn Lys Thr Pro Asp Lys Leu Gln Gln Ala
                     165                 170                 175

      Ala Leu Pro Leu Leu Ser Asn Ala Glu Cys Lys Lys Ser Trp Gly Arg
                 180                 185                 190

      Arg Ile Thr Asp Val Met Ile Cys Ala Gly Ala Ser Gly Val Ser Ser
  20         195                 200                 205

      Cys Met Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Lys Asp Gly Ala
                 210                 215                 220

      Trp Thr Leu Val Gly Ile Val Ser Trp Gly Ser Asp Thr Cys Ser Thr
      225                 230                 235                 240
```

Ser Ser Pro Gly Val Tyr Ala Arg Val Thr Lys Leu Ile Pro Trp Val

                245   250   255

Gln Lys Ile Leu Ala Ala Asn

            260

5

<210> 75

<211> 247

<212> PRT

10 <213> Homo sapiens

<220>

<221> Trypsin I precursor

<222> (1)..(247)

<223> Accession No. as of 29 August 2003: P07477

15 <400> 75

Met Asn Pro Leu Leu Ile Leu Thr Phe Val Ala Ala Ala Leu Ala Ala

1   5   10   15

Pro Phe Asp Asp Asp Asp Lys Ile Val Gly Gly Tyr Asn Cys Glu Glu

20   20   25   30

Asn Ser Val Pro Tyr Gln Val Ser Leu Asn Ser Gly Tyr His Phe Cys

                35   40   45

Gly Gly Ser Leu Ile Asn Glu Gln Trp Val Val Ser Ala Gly His Cys

            50   55   60

Tyr Lys Ser Arg Ile Gln Val Arg Leu Gly Glu His Asn Ile Glu Val

65   70   75   80

Leu Glu Gly Asn Glu Gln Phe Ile Asn Ala Ala Lys Ile Ile Arg His

                        85   90   95

5   Pro Gln Tyr Asp Arg Lys Thr Leu Asn Asn Asp Ile Met Leu Ile Lys

                        100   105   110

Leu Ser Ser Arg Ala Val Ile Asn Ala Arg Val Ser Thr Ile Ser Leu

                115   120   125

Pro Thr Ala Pro Pro Ala Thr Gly Thr Lys Cys Leu Ile Ser Gly Trp

10   130   135   140

Gly Asn Thr Ala Ser Ser Gly Ala Asp Tyr Pro Asp Glu Leu Gln Cys

145   150   155   160

Leu Asp Ala Pro Val Leu Ser Gln Ala Lys Cys Glu Ala Ser Tyr Pro

                        165   170   175

15   Gly Lys Ile Thr Ser Asn Met Phe Cys Val Gly Phe Leu Glu Gly Gly

                        180   185   190

Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Val Val Cys Asn Gly

                195   200   205

Gln Leu Gln Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln Lys Asn

20   210   215   220

Lys Pro Gly Val Tyr Thr Lys Val Tyr Asn Tyr Val Lys Trp Ile Lys

225   230   235   240

Asn Thr Ile Ala Ala Asn Ser

                245

<210> 76

<211> 247

5   <212> PRT

<213> Homo sapiens

<220>

<221> Trypsin II precursor

<222> (1)..(247)

10   <223> Accession No. as of 29 August 2003: P07478

<400> 76

Met Asn Leu Leu Leu Ile Leu Thr Phe Val Ala Ala Ala Val Ala Ala

1   5   10   15

15   Pro Phe Asp Asp Asp Asp Lys Ile Val Gly Gly Tyr Ile Cys Glu Glu

                 20   25   30

Asn Ser Val Pro Tyr Gln Val Ser Leu Asn Ser Gly Tyr His Phe Cys

                 35   40   45

Gly Gly Ser Leu Ile Ser Glu Gln Trp Val Val Ser Ala Gly His Cys

20   50   55   60

Tyr Lys Ser Arg Ile Gln Val Arg Leu Gly Glu His Asn Ile Glu Val

65   70   75   80

Leu Glu Gly Asn Glu Gln Phe Ile Asn Ala Ala Lys Ile Ile Arg His

                 85   90   95

Pro Lys Tyr Asn Ser Arg Thr Leu Asp Asn Asp Ile Leu Leu Ile Lys
              100   105   110

Leu Ser Ser Pro Ala Val Ile Asn Ser Arg Val Ser Ala Ile Ser Leu
              115   120   125

5   Pro Thr Ala Pro Pro Ala Ala Gly Thr Glu Ser Leu Ile Ser Gly Trp
              130   135   140

Gly Asn Thr Leu Ser Ser Gly Ala Asp Tyr Pro Asp Glu Leu Gln Cys
     145   150   155   160

Leu Asp Ala Pro Val Leu Ser Gln Ala Glu Cys Glu Ala Ser Tyr Pro
10   165   170   175

Gly Lys Ile Thr Asn Asn Met Phe Cys Val Gly Phe Leu Glu Gly Gly
              180   185   190

Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Val Val Ser Asn Gly
              195   200   205

15   Glu Leu Gln Gly Ile Val Ser Trp Gly Tyr Gly Cys Ala Gln Lys Asn
              210   215   220

Arg Pro Gly Val Tyr Thr Lys Val Tyr Asn Tyr Val Asp Trp Ile Lys
     225   230   235   240

Asp Thr Ile Ala Ala Asn Ser
20   245

     <210> 77

     <211> 379

```
<212>   PRT

<213>   Homo sapiens

<220>

<221>   Leukocyte elastase inhibitor (LEI)

<222>   (1)..(379)

<223>   Accession No. as of 29 August 2003: P30740

<400>   77
```

```
Met Gln Leu Ser Ser Ala Asn Thr Arg Phe Ala Leu Asp Leu Phe
1               5                   10                  15

Leu Ala Leu Ser Glu Asn Asn Pro Ala Gly Asn Ile Phe Ile Ser Pro
            20                  25                  30

Phe Ser Ile Ser Ser Ala Met Ala Met Val Phe Leu Gly Thr Arg Gly
            35                  40                  45

Asn Thr Ala Ala Gln Leu Ser Lys Thr Phe His Phe Asn Thr Val Glu
        50                  55                  60

Glu Val His Ser Arg Phe Gln Ser Leu Asn Ala Asp Ile Asn Lys Arg
65                  70                  75                  80

Gly Ala Ser Tyr Ile Leu Lys Leu Ala Asn Arg Leu Tyr Gly Glu Lys
                85                  90                  95

Thr Tyr Asn Phe Leu Pro Glu Phe Leu Val Ser Thr Gln Lys Thr Tyr
                100                 105                 110

Gly Ala Asp Leu Ala Ser Val Asp Phe Gln His Ala Ser Glu Asp Ala
                115                 120                 125
```

Arg Lys Thr Ile Asn Gln Trp Val Lys Gly Gln Thr Glu Gly Lys Ile
        130   135   140

Pro Glu Leu Leu Ala Ser Gly Met Val Asp Asn Met Thr Lys Leu Val
        145   150   155   160

5   Leu Val Asn Ala Ile Tyr Phe Lys Gly Asn Trp Lys Asp Lys Phe Met
                    165   170   175

Lys Glu Ala Thr Thr Asn Ala Pro Phe Arg Leu Asn Lys Lys Asp Arg
                180   185   190

Lys Thr Val Lys Met Met Tyr Gln Lys Lys Lys Phe Ala Tyr Gly Tyr
10   195   200   205

Ile Glu Asp Leu Lys Cys Arg Val Leu Glu Leu Pro Tyr Gln Gly Glu
        210   215   220

Glu Leu Ser Met Val Ile Leu Leu Pro Asp Asp Ile Glu Asp Glu Ser
    225   230   235   240

15 Thr Gly Leu Lys Lys Ile Glu Glu Gln Leu Thr Leu Glu Lys Leu His
                    245   250   255

Glu Trp Thr Lys Pro Glu Asn Leu Asp Phe Ile Glu Val Asn Val Ser
                260   265   270

Leu Pro Arg Phe Lys Leu Glu Glu Ser Tyr Thr Leu Asn Ser Asp Leu
20   275   280   285

Ala Arg Leu Gly Val Gln Asp Leu Phe Asn Ser Ser Lys Ala Asp Leu
        290   295   300

Ser Gly Met Ser Gly Ala Arg Asp Ile Phe Ile Ser Lys Ile Val His
    305   310   315   320

Lys Ser Phe Val Glu Val Asn Glu Glu Gly Thr Glu Ala Ala Ala Ala
                    325   330   335

Thr Ala Gly Ile Ala Thr Phe Cys Met Leu Met Pro Glu Glu Asn Phe
                    340   345   350

5   Thr Ala Asp His Pro Phe Leu Phe Phe Ile Arg His Asn Ser Ser Gly
                    355   360   365

Ser Ile Leu Phe Leu Gly Arg Phe Ser Ser Pro
            370   375

10

    <210>   78

    <211>   573

    <212>   PRT

    <213>   Homo sapiens

15 <220>

    <221>   Hsp60

    <222>   (1)..(573)

    <223>   Accession No. as of 29 August 2003: P10809

    <400>   78

20

    Met Leu Arg Leu Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser Arg
    1   5   10   15

    Val Leu Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe
                    20   25   30

Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala
            35   40   45

Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg Thr Val Ile Ile
            50   55   60

5 Glu Gln Ser Trp Gly Ser Pro Lys Val Thr Lys Asp Gly Val Thr Val
   65   70   75   80

Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys
                  85   90   95

Leu Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu Ala Gly Asp Gly
10   100   105   110

Thr Thr Thr Ala Thr Val Leu Ala Arg Ser Ile Ala Lys Glu Gly Phe
                  115   120   125

Glu Lys Ile Ser Lys Gly Ala Asn Pro Val Glu Ile Arg Arg Gly Val
            130   135   140

15 Met Leu Ala Val Asp Ala Val Ile Ala Glu Leu Lys Lys Gln Ser Lys
    145   150   155   160

Pro Val Thr Thr Pro Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala
                  165   170   175

Asn Gly Asp Lys Glu Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys
20   180   185   190

Val Gly Arg Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn
            195   200   205

Asp Glu Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile
            210   215   220

Ser Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln

225   230   235   240

Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Ile Gln Ser

                       245   250   255

5 Ile Val Pro Ala Leu Glu Ile Ala Asn Ala His Arg Lys Pro Leu Val

                       260   265   270

Ile Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr Leu Val Leu

                       275   280   285

Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val Lys Ala Pro Gly

10   290   295   300

Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp Met Ala Ile Ala Thr

305   310   315   320

Gly Gly Ala Val Phe Gly Glu Glu Gly Leu Thr Leu Asn Leu Glu Asp

                       325   330   335

15 Val Gln Pro His Asp Leu Gly Lys Val Gly Glu Val Ile Val Thr Lys

                       340   345   350

Asp Asp Ala Met Leu Leu Lys Gly Lys Gly Asp Lys Ala Gln Ile Glu

        355   360   365

Lys Arg Ile Gln Glu Ile Ile Glu Gln Leu Asp Val Thr Thr Ser Glu

20   370   375   380

Tyr Glu Lys Glu Lys Leu Asn Glu Arg Leu Ala Lys Leu Ser Asp Gly

385   390   395   400

Val Ala Val Leu Lys Val Gly Gly Thr Ser Asp Val Glu Val Asn Glu

                       405   410   415

Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala Val

          420   425   430

Glu Glu Gly Ile Val Leu Gly Gly Cys Ala Leu Leu Arg Cys Ile

          435   440   445

5   Pro Ala Leu Asp Ser Leu Thr Pro Ala Asn Glu Asp Gln Lys Ile Gly

          450   455   460

Ile Glu Ile Ile Lys Arg Thr Leu Lys Ile Pro Ala Met Thr Ile Ala

    465   470   475   480

Lys Asn Ala Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Met Gln

10   485   490   495

Ser Ser Ser Glu Val Gly Tyr Asp Ala Met Ala Gly Asp Phe Val Asn

                    500   505   510

Met Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val Arg Thr Ala

              515   520   525

15 Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr Thr Ala Glu Val

          530   535   540

Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp Pro Gly Met Gly Ala

    545   550   555   560

Met Gly Gly Met Gly Gly Gly Met Gly Gly Gly Met Phe

20   565   570

<210>   79

<211>   803

<212>   PRT

<213>   Homo sapiens

<220>

<221>   Endoplasmin precursor (GRP94)

5   <222>   (1)..(803)

<223>   Accession No. as of 29 August 2003: P14625

<400>   79


```
     Met Arg Ala Leu Trp Val Leu Gly Leu Cys Cys Val Leu Leu Thr Phe
10   1               5                   10                  15

     Gly Ser Val Arg Ala Asp Asp Glu Val Asp Val Asp Gly Thr Val Glu
                     20                  25                  30

     Glu Asp Leu Gly Lys Ser Arg Glu Gly Ser Arg Thr Asp Asp Glu Val
                     35                  40                  45

15   Val Gln Arg Glu Glu Glu Ala Ile Gln Leu Asp Gly Leu Asn Ala Ser
                 50                  55                  60

     Gln Ile Arg Glu Leu Arg Glu Lys Ser Glu Lys Phe Ala Phe Gln Ala
     65                  70                  75                  80

     Glu Val Asn Arg Met Met Lys Leu Ile Ile Asn Ser Leu Tyr Lys Asn
20                   85                  90                  95

     Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ala Ser Asp Ala Leu
                     100                 105                 110

     Asp Lys Ile Arg Leu Ile Ser Leu Thr Asp Glu Asn Ala Leu Ser Gly
                     115                 120                 125
```

```
        Asn Glu Glu Leu Thr Val Lys Ile Lys Cys Asp Lys Glu Lys Asn Leu
            130                 135                 140

        Leu His Val Thr Asp Thr Gly Val Gly Met Thr Arg Glu Glu Leu Val
            145                 150                 155                 160

    5   Lys Asn Leu Gly Thr Ile Ala Lys Ser Gly Thr Ser Glu Phe Leu Asn
                                165                 170                 175

        Lys Met Thr Glu Ala Gln Glu Asp Gly Gln Ser Thr Ser Glu Leu Ile
                    180                 185                 190

        Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Phe Leu Val Ala Asp Lys
   10           195                 200                 205

        Val Ile Val Thr Ser Lys His Asn Asn Asp Thr Gln His Ile Trp Glu
                    210                 215                 220

        Ser Asp Ser Asn Glu Phe Ser Val Ile Ala Asp Pro Arg Gly Asn Thr
            225                 230                 235                 240

   15   Leu Gly Arg Gly Thr Thr Ile Thr Leu Val Leu Lys Glu Glu Ala Ser
                            245                 250                 255

        Asp Tyr Leu Glu Leu Asp Thr Ile Lys Asn Leu Val Lys Lys Tyr Ser
                    260                 265                 270

        Gln Phe Ile Asn Phe Pro Ile Tyr Val Trp Ser Ser Lys Thr Glu Thr
   20           275                 280                 285

        Val Glu Glu Pro Met Glu Glu Glu Ala Ala Lys Glu Glu Lys Glu
            290                 295                 300

        Glu Ser Asp Asp Glu Ala Ala Val Glu Glu Glu Glu Glu Lys Lys
        305                 310                 315                 320
```

Pro Lys Thr Lys Lys Val Glu Lys Thr Val Trp Asp Trp Glu Leu Met

            325   330   335

Asn Asp Ile Lys Pro Ile Trp Gln Arg Pro Ser Lys Glu Val Glu Glu

            340   345   350

5   Asp Glu Tyr Lys Ala Phe Tyr Lys Ser Phe Ser Lys Glu Ser Asp Asp

            355   360   365

Pro Met Ala Tyr Ile His Phe Thr Ala Glu Gly Glu Val Thr Phe Lys

            370   375   380

Ser Ile Leu Phe Val Pro Thr Ser Ala Pro Arg Gly Leu Phe Asp Glu

10 385   390   395   400

Tyr Gly Ser Lys Lys Ser Asp Tyr Ile Lys Leu Tyr Val Arg Arg Val

            405   410   415

Phe Ile Thr Asp Asp Phe His Asp Met Met Pro Lys Tyr Leu Asn Phe

            420   425   430

15 Val Lys Gly Val Val Asp Ser Asp Asp Leu Pro Leu Asn Val Ser Arg

            435   440   445

Glu Thr Leu Gln Gln His Lys Leu Leu Lys Val Ile Arg Lys Lys Leu

            450   455   460

Val Arg Lys Thr Leu Asp Met Ile Lys Lys Ile Ala Asp Asp Lys Tyr

20 465   470   475   480

Asn Asp Thr Phe Trp Lys Glu Phe Gly Thr Asn Ile Lys Leu Gly Val

            485   490   495

Ile Glu Asp His Ser Asn Arg Thr Arg Leu Ala Lys Leu Leu Arg Phe

            500   505   510

Gln Ser Ser His His Pro Thr Asp Ile Thr Ser Leu Asp Gln Tyr Val

        515   520   525

Glu Arg Met Lys Glu Lys Gln Asp Lys Ile Tyr Phe Met Ala Gly Ser

        530   535   540

5 Ser Arg Lys Glu Ala Glu Ser Ser Pro Phe Val Glu Arg Leu Leu Lys

   545   550   555   560

Lys Gly Tyr Glu Val Ile Tyr Leu Thr Glu Pro Val Asp Glu Tyr Cys

                565   570   575

Ile Gln Ala Leu Pro Glu Phe Asp Gly Lys Arg Phe Gln Asn Val Ala

10   580   585   590

Lys Glu Gly Val Lys Phe Asp Glu Ser Glu Lys Thr Lys Glu Ser Arg

                595   600   605

Glu Ala Val Glu Lys Glu Phe Glu Pro Leu Leu Asn Trp Met Lys Asp

        610   615   620

15 Lys Ala Leu Lys Asp Lys Ile Glu Lys Ala Val Val Ser Gln Arg Leu

   625   630   635   640

Thr Glu Ser Pro Cys Ala Leu Val Ala Ser Gln Tyr Gly Trp Ser Gly

                645   650   655

Asn Met Glu Arg Ile Met Lys Ala Gln Ala Tyr Gln Thr Gly Lys Asp

20   660   665   670

Ile Ser Thr Asn Tyr Tyr Ala Ser Gln Lys Lys Thr Phe Glu Ile Asn

                675   680   685

Pro Arg His Pro Leu Ile Arg Asp Met Leu Arg Arg Ile Lys Glu Asp

        690   695   700

Glu Asp Asp Lys Thr Val Leu Asp Leu Ala Val Val Leu Phe Glu Thr

705   710   715   720

Ala Thr Leu Arg Ser Gly Tyr Leu Leu Pro Asp Thr Lys Ala Tyr Gly

                725   730   735

5   Asp Arg Ile Glu Arg Met Leu Arg Leu Ser Leu Asn Ile Asp Pro Asp

                740   745   750

Ala Lys Val Glu Glu Glu Pro Glu Glu Glu Pro Glu Glu Thr Ala Glu

        755   760   765

Asp Thr Thr Glu Asp Thr Glu Gln Asp Glu Asp Glu Glu Met Asp Val

10   770   775   780

Gly Thr Asp Glu Glu Glu Glu Thr Ala Lys Glu Ser Thr Ala Glu Lys

785   790   795   800

Asp Glu Leu

15

<210> 80

<211> 261

<212> PRT

20   <213> Homo sapiens

<220>

<221> Endoplasmic reticulum protein ERp29 precursor (ERp31) (ERp28)

<222> (1)..(261)

<223> Accession No. as of 29 August 2003: P30040

<400>   80

Met Ala Ala Ala Val Pro Arg Ala Ala Phe Leu Ser Pro Leu Leu Pro
1   5   10   15

5 Leu Leu Leu Gly Phe Leu Leu Leu Ser Ala Pro His Gly Gly Ser Gly
               20   25   30

Leu His Thr Lys Gly Ala Leu Pro Leu Asp Thr Val Thr Phe Tyr Lys
               35   40   45

Val Ile Pro Lys Ser Lys Phe Val Leu Val Lys Phe Asp Thr Gln Tyr
10   50   55   60

Pro Tyr Gly Glu Lys Gln Asp Glu Phe Lys Arg Leu Ala Glu Asn Ser
65   70   75   80

Ala Ser Ser Asp Asp Leu Leu Val Ala Glu Val Gly Ile Ser Asp Tyr
                   85   90   95

15 Gly Asp Lys Leu Asn Met Glu Leu Ser Glu Lys Tyr Lys Leu Asp Lys
                  100   105   110

Glu Ser Tyr Pro Val Phe Tyr Leu Phe Arg Asp Gly Asp Phe Glu Asn
                  115   120   125

Pro Val Pro Tyr Thr Gly Ala Val Lys Val Gly Ala Ile Gln Arg Trp
20   130   135   140

Leu Lys Gly Gln Gly Val Tyr Leu Gly Met Pro Gly Cys Leu Pro Val
145   150   155   160

Tyr Asp Ala Leu Ala Gly Glu Phe Ile Arg Ala Ser Gly Val Glu Ala
                  165   170   175

```
Arg Gln Ala Leu Leu Lys Gln Gly Gln Asp Asn Leu Ser Ser Val Lys
            180                 185                 190

Glu Thr Gln Lys Lys Trp Ala Glu Gln Tyr Leu Lys Ile Met Gly Lys
            195                 200                 205

5  Ile Leu Asp Gln Gly Glu Asp Phe Pro Ala Ser Glu Met Thr Arg Ile
            210                 215                 220

Ala Arg Leu Ile Glu Lys Asn Lys Met Ser Asp Gly Lys Lys Glu Glu
225                 230                 235                 240

Leu Gln Lys Ser Leu Asn Ile Leu Thr Ala Phe Gln Lys Lys Gly Ala
10                 245                 250                 255

Glu Lys Glu Glu Leu
            260
```

```
15  <210>  81

    <211>  525

    <212>  PRT

    <213>  Homo sapiens

    <220>

20  <221>  Protein disulfide isomerase A2 precursor

    <222>  (1)..(525)

    <223>  Accession No. as of 29 August 2003: Q13087

    <400>  81
```

```
      Met Ser Arg Gln Leu Leu Pro Val Leu Leu Leu Leu Leu Arg Ala
      1               5               10              15

      Ser Cys Pro Trp Gly Gln Glu Gln Gly Ala Arg Ser Pro Ser Glu Glu
                  20              25              30

  5   Pro Pro Glu Glu Glu Ile Pro Lys Glu Asp Gly Ile Leu Val Leu Ser
                  35              40              45

      Arg His Thr Leu Gly Leu Ala Leu Arg Glu His Pro Ala Leu Leu Val
                  50              55              60

      Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Gln Ala Leu Ala Pro Glu
 10   65              70              75              80

      Tyr Ser Lys Ala Ala Ala Val Leu Ala Ala Glu Ser Met Val Val Thr
                  85              90              95

      Leu Ala Lys Val Asp Gly Pro Ala Gln Arg Glu Leu Ala Glu Glu Phe
                  100             105             110

 15   Gly Val Thr Glu Tyr Pro Thr Leu Lys Phe Phe Arg Asn Gly Asn Arg
                  115             120             125

      Thr His Pro Glu Glu Tyr Thr Gly Pro Arg Asp Ala Glu Gly Ile Ala
                  130             135             140

      Glu Trp Leu Arg Arg Arg Val Gly Pro Ser Ala Met Arg Leu Glu Asp
 20   145             150             155             160

      Glu Ala Ala Ala Gln Ala Leu Ile Gly Gly Arg Asp Leu Val Val Ile
                  165             170             175

      Gly Phe Phe Gln Asp Leu Gln Asp Glu Asp Val Ala Thr Phe Leu Ala
                  180             185             190
```

Leu Ala Gln Asp Ala Leu Asp Met Thr Phe Gly Leu Thr Asp Arg Pro
            195   200   205

Arg Leu Phe Gln Gln Phe Gly Leu Thr Lys Asp Thr Val Val Leu Phe
        210   215   220

5   Lys Lys Phe Asp Glu Gly Arg Ala Asp Phe Pro Val Asp Glu Glu Leu
        225   230   235   240

Gly Leu Asp Leu Gly Asp Leu Ser Arg Phe Leu Val Thr His Ser Met
                245   250   255

Arg Leu Val Thr Glu Phe Asn Ser Gln Thr Ser Ala Lys Ile Phe Ala
10   260   265   270

Ala Arg Ile Leu Asn His Leu Leu Leu Phe Val Asn Gln Thr Leu Ala
            275   280   285

Ala His Arg Glu Leu Leu Ala Gly Phe Gly Glu Ala Ala Pro Arg Phe
            290   295   300

15 Arg Gly Gln Val Leu Phe Val Val Val Asp Val Ala Ala Asp Asn Glu
    305   310   315   320

His Val Leu Gln Tyr Phe Gly Leu Lys Ala Glu Ala Ala Pro Thr Leu
                325   330   335

Arg Leu Val Asn Leu Glu Thr Thr Lys Lys Tyr Ala Pro Val Asp Gly
20   340   345   350

Gly Pro Val Thr Ala Ala Ser Ile Thr Ala Phe Cys His Ala Val Leu
            355   360   365

Asn Gly Gln Val Lys Pro Tyr Leu Leu Ser Gln Glu Ile Pro Pro Asp
            370   375   380

Trp Asp Gln Arg Pro Val Lys Thr Leu Val Gly Lys Asn Phe Glu Gln

385   390   395   400

Val Ala Phe Asp Glu Thr Lys Asn Val Phe Val Lys Phe Tyr Ala Pro

                405   410   415

5   Trp Cys Thr His Cys Lys Glu Met Ala Pro Ala Trp Glu Ala Leu Ala

                420   425   430

Glu Lys Tyr Gln Asp His Glu Asp Ile Ile Ile Ala Glu Leu Asp Ala

                435   440   445

Thr Ala Asn Glu Leu Asp Ala Phe Ala Val His Gly Phe Pro Thr Leu

10   450   455   460

Lys Tyr Phe Pro Ala Gly Pro Gly Arg Lys Val Ile Glu Tyr Lys Ser

465   470   475   480

Thr Arg Asp Leu Glu Thr Phe Ser Lys Phe Leu Asp Asn Gly Gly Val

                485   490   495

15   Leu Pro Thr Glu Glu Pro Pro Glu Glu Pro Ala Ala Pro Phe Pro Glu

                500   505   510

Pro Pro Ala Asn Ser Thr Met Gly Ser Lys Glu Glu Leu

                515   520   525

20

<210> 82

<211> 505

<212> PRT

<213> Homo sapiens

<220>

<221>   Protein disulfide isomerase A3 precursor

<222>   (1)..(505)

<223>   Accession No. as of 29 August 2003: P30101

5   <400>   82

Met Arg Leu Arg Arg Leu Ala Leu Phe Pro Gly Val Ala Leu Leu Leu
1   5   10   15

Ala Ala Ala Arg Leu Ala Ala Ala Ser Asp Val Leu Glu Leu Thr Asp
10   20   25   30

Asp Asn Phe Glu Ser Arg Ile Ser Asp Thr Gly Ser Ala Gly Leu Met
                35   40   45

Leu Val Glu Phe Phe Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala
                50   55   60

15 Pro Glu Tyr Glu Ala Ala Ala Thr Arg Leu Lys Gly Ile Val Pro Leu
    65   70   75   80

Ala Lys Val Asp Cys Thr Ala Asn Thr Asn Thr Cys Asn Lys Tyr Gly
                85   90   95

Val Ser Gly Tyr Pro Thr Leu Lys Ile Phe Arg Asp Gly Glu Glu Ala
20   100   105   110

Gly Ala Tyr Asp Gly Pro Arg Thr Ala Asp Gly Ile Val Ser His Leu
                115   120   125

Lys Lys Gln Ala Gly Pro Ala Ser Val Pro Leu Arg Thr Glu Glu Glu
                130   135   140

Phe Lys Lys Phe Ile Ser Asp Lys Asp Ala Ser Ile Val Gly Phe Phe
145   150   155   160

Asp Asp Ser Phe Ser Glu Ala His Ser Glu Phe Leu Lys Ala Ala Ser
                165   170   175

5   Asn Leu Arg Asp Asn Tyr Arg Phe Ala His Thr Asn Val Glu Ser Leu
                180   185   190

Val Asn Glu Tyr Asp Asp Asn Gly Glu Gly Ile Ile Leu Phe Arg Pro
            195   200   205

Ser His Leu Thr Asn Lys Phe Glu Asp Lys Thr Val Ala Tyr Thr Glu
10   210   215   220

Gln Lys Met Thr Ser Gly Lys Ile Lys Lys Phe Ile Gln Glu Asn Ile
225   230   235   240

Phe Gly Ile Cys Pro His Met Thr Glu Asp Asn Lys Asp Leu Ile Gln
                245   250   255

15 Gly Lys Asp Leu Leu Ile Ala Tyr Tyr Asp Val Asp Tyr Glu Lys Asn
                260   265   270

Ala Lys Gly Ser Asn Tyr Trp Arg Asn Arg Val Met Met Val Ala Lys
            275   280   285

Lys Phe Leu Asp Ala Gly His Lys Leu Asn Phe Ala Val Ala Ser Arg
20   290   295   300

Lys Thr Phe Ser His Glu Leu Ser Asp Phe Gly Leu Glu Ser Thr Ala
305   310   315   320

Gly Glu Ile Pro Val Val Ala Ile Arg Thr Ala Lys Gly Glu Lys Phe
                325   330   335

Val Met Gln Glu Glu Phe Ser Arg Asp Gly Lys Ala Leu Glu Arg Phe
        340   345   350

Leu Gln Asp Tyr Phe Asp Gly Asn Leu Lys Arg Tyr Leu Lys Ser Glu
        355   360   365

5   Pro Ile Pro Glu Ser Asn Asp Gly Pro Val Lys Val Val Ala Glu
        370   375   380

Asn Phe Asp Glu Ile Val Asn Asn Glu Asn Lys Asp Val Leu Ile Glu
    385   390   395   400

Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Asn Leu Glu Pro Lys Tyr
10   405   410   415

Lys Glu Leu Gly Glu Lys Leu Ser Lys Asp Pro Asn Ile Val Ile Ala
            420   425   430

Lys Met Asp Ala Thr Ala Asn Asp Val Pro Ser Pro Tyr Glu Val Arg
        435   440   445

15 Gly Phe Pro Thr Ile Tyr Phe Ser Pro Ala Asn Lys Lys Leu Asn Pro
        450   455   460

Lys Lys Tyr Glu Gly Gly Arg Glu Leu Ser Asp Phe Ile Ser Tyr Leu
    465   470   475   480

Gln Arg Glu Ala Thr Asn Pro Pro Val Ile Gln Glu Glu Lys Pro Lys
20   485   490   495

Lys Lys Lys Lys Ala Gln Glu Asp Leu
        500   505

<210> 83

<211> 374

<212> PRT

<213> Homo sapiens

5 <220>

<221> Alcohol dehydrogenase beta chain

<222> (1)..(374)

<223> Accession No. as of 29 August 2003: P00325

<400> 83

10

Ser Thr Ala Gly Lys Val Ile Lys Cys Lys Ala Ala Val Leu Trp Glu
1   5   10   15

Val Lys Lys Pro Phe Ser Ile Glu Asp Val Glu Val Ala Pro Pro Lys
                20   25   30

15 Ala Tyr Glu Val Arg Ile Lys Met Val Ala Val Gly Ile Cys Arg Thr
                35   40   45

Asp Asp His Val Val Ser Gly Asn Leu Val Thr Pro Leu Pro Val Ile
        50   55   60

Leu Gly His Glu Ala Ala Gly Ile Val Glu Ser Val Gly Glu Gly Val
20 65   70   75   80

Thr Thr Val Lys Pro Gly Asp Lys Val Ile Pro Leu Phe Thr Pro Gln
                85   90   95

Cys Gly Lys Cys Arg Val Cys Lys Asn Pro Glu Ser Asn Tyr Cys Leu
                100   105   110

Lys Asn Asp Leu Gly Asn Pro Arg Gly Thr Leu Gln Asp Gly Thr Arg

     115   120   125

Arg Phe Thr Cys Arg Gly Lys Pro Ile His His Phe Leu Gly Thr Ser

     130   135   140

5   Thr Phe Ser Gln Tyr Thr Val Val Asp Glu Asn Ala Val Ala Lys Ile

     145   150   155   160

Asp Ala Ala Ser Pro Leu Glu Lys Val Cys Leu Ile Gly Cys Gly Phe

          165   170   175

Ser Thr Gly Tyr Gly Ser Ala Val Asn Val Ala Lys Val Thr Pro Gly

10   180   185   190

Ser Thr Cys Ala Val Phe Gly Leu Gly Gly Val Gly Leu Ser Ala Val

     195   200   205

Met Gly Cys Lys Ala Ala Gly Ala Ala Arg Ile Ile Ala Val Asp Ile

     210   215   220

15 Asn Lys Asp Lys Phe Ala Lys Ala Lys Glu Leu Gly Ala Thr Glu Cys

225   230   235   240

Ile Asn Pro Gln Asp Tyr Lys Lys Pro Ile Gln Glu Val Leu Lys Glu

          245   250   255

Met Thr Asp Gly Gly Val Asp Phe Ser Phe Glu Val Ile Gly Arg Leu

20   260   265   270

Asp Thr Met Met Ala Ser Leu Leu Cys Cys His Glu Ala Cys Gly Thr

     275   280   285

Ser Val Ile Val Gly Val Pro Pro Ala Ser Gln Asn Leu Ser Ile Asn

     290   295   300

Pro Met Leu Leu Leu Thr Gly Arg Thr Trp Lys Gly Ala Val Tyr Gly

305   310   315   320

Gly Phe Lys Ser Lys Glu Gly Ile Pro Lys Leu Val Ala Asp Phe Met

                  325   330   335

5   Ala Lys Lys Phe Ser Leu Asp Ala Leu Ile Thr His Val Leu Pro Phe

                  340   345   350

Glu Lys Ile Asn Glu Gly Phe Asp Leu Leu His Ser Gly Lys Ser Ile

                  355   360   365

Arg Thr Val Leu Thr Phe

10   370

    <210>   84

    <211>   241

15 <212>   PRT

    <213>   Homo sapiens

    <220>

    <221>   Glutathione transferase omega 1

    <222>   (1)..(241)

20 <223>   Accession No. as of 29 August 2003: P78417

    <400>   84

Met Ser Gly Glu Ser Ala Arg Ser Leu Gly Lys Gly Ser Ala Pro Pro

1   5   10   15

```
      Gly Pro Val Pro Glu Gly Ser Ile Arg Ile Tyr Ser Met Arg Phe Cys
                   20                25                30

      Pro Phe Ala Glu Arg Thr Arg Leu Val Leu Lys Ala Lys Gly Ile Arg
                   35                40                45

   5  His Glu Val Ile Asn Ile Asn Leu Lys Asn Lys Pro Glu Trp Phe Phe
                   50                55                60

      Lys Lys Asn Pro Phe Gly Leu Val Pro Val Leu Glu Asn Ser Gln Gly
      65                70                75                80

      Gln Leu Ile Tyr Glu Ser Ala Ile Thr Cys Glu Tyr Leu Asp Glu Ala
  10                   85                90                95

      Tyr Pro Gly Lys Lys Leu Leu Pro Asp Asp Pro Tyr Glu Lys Ala Cys
                   100               105               110

      Gln Lys Met Ile Leu Glu Leu Phe Ser Lys Val Pro Ser Leu Val Gly
                   115               120               125

  15  Ser Phe Ile Arg Ser Gln Asn Lys Glu Asp Tyr Ala Gly Leu Lys Glu
                   130               135               140

      Glu Phe Arg Lys Glu Phe Thr Lys Leu Glu Glu Val Leu Thr Asn Lys
      145               150               155               160

      Lys Thr Thr Phe Phe Gly Gly Asn Ser Ile Ser Met Ile Asp Tyr Leu
  20                   165               170               175

      Ile Trp Pro Trp Phe Glu Arg Leu Glu Ala Met Lys Leu Asn Glu Cys
                   180               185               190

      Val Asp His Thr Pro Lys Leu Lys Leu Trp Met Ala Ala Met Lys Glu
                   195               200               205
```

Asp Pro Thr Val Ser Ala Leu Leu Thr Ser Glu Lys Asp Trp Gln Gly

        210   215   220

Phe Leu Glu Leu Tyr Leu Gln Asn Ser Pro Glu Ala Cys Asp Tyr Gly

        225   230   235   240

5   Leu

    <210>   85

10 <211>   999

    <212>   PRT

    <213>   Homo sapiens

    <220>

    <221>   150 kDa oxygen-regulated protein precursor (Orp150)

15 <222>   (1)..(999)

    <223>   Accession No. as of 29 August 2003: Q9Y4L1

    <400>   85

    Met Ala Asp Lys Val Arg Arg Gln Arg Pro Arg Arg Arg Val Cys Trp

20 1   5   10   15

    Ala Leu Val Ala Val Leu Leu Ala Asp Leu Leu Ala Leu Ser Asp Thr

                20   25   30

    Leu Ala Val Met Ser Val Asp Leu Gly Ser Glu Ser Met Lys Val Ala

            35   40   45

```
        Ile Val Lys Pro Gly Val Pro Met Glu Ile Val Leu Asn Lys Glu Ser
                50              55              60

        Arg Arg Lys Thr Pro Val Ile Val Thr Leu Lys Glu Asn Glu Arg Phe
        65              70              75              80

  5     Phe Gly Asp Ser Ala Ala Ser Met Ala Ile Lys Asn Pro Lys Ala Thr
                        85              90              95

        Leu Arg Tyr Phe Gln His Leu Leu Gly Lys Gln Ala Asp Asn Pro His
                        100             105             110

        Val Ala Leu Tyr Gln Ala Arg Phe Pro Glu His Glu Leu Thr Phe Asp
  10            115             120             125

        Pro Gln Arg Gln Thr Val His Phe Gln Ile Ser Ser Gln Leu Gln Phe
                130             135             140

        Ser Pro Glu Glu Val Leu Gly Met Val Leu Asn Tyr Ser Arg Ser Leu
        145             150             155             160

  15    Ala Glu Asp Phe Ala Glu Gln Pro Ile Lys Asp Ala Val Ile Thr Val
                        165             170             175

        Pro Val Phe Phe Asn Gln Ala Glu Arg Arg Ala Val Leu Gln Ala Ala
                        180             185             190

        Arg Met Ala Gly Leu Lys Val Leu Gln Leu Ile Asn Asp Asn Thr Ala
  20            195             200             205

        Thr Ala Leu Ser Tyr Gly Val Phe Arg Arg Lys Asp Ile Asn Thr Thr
                210             215             220

        Ala Gln Asn Ile Met Phe Tyr Asp Met Gly Ser Gly Ser Thr Val Cys
        225             230             235             240
```

Thr Ile Val Thr Tyr Gln Met Val Lys Thr Lys Glu Ala Gly Met Gln
                  245   250   255

Pro Gln Leu Gln Ile Arg Gly Val Gly Phe Asp Arg Thr Leu Gly Gly
                  260   265   270

5 Leu Glu Met Glu Leu Arg Leu Arg Glu Arg Leu Ala Gly Leu Phe Asn
                  275   280   285

Glu Gln Arg Lys Gly Gln Arg Ala Lys Asp Val Arg Glu Asn Pro Arg
               290   295   300

Ala Met Ala Lys Leu Leu Arg Glu Ala Asn Arg Leu Lys Thr Val Leu
10 305   310   315   320

Ser Ala Asn Ala Asp His Met Ala Gln Ile Glu Gly Leu Met Asp Asp
                  325   330   335

Val Asp Phe Lys Ala Lys Val Thr Arg Val Glu Phe Glu Glu Leu Cys
                  340   345   350

15 Ala Asp Leu Phe Glu Arg Val Pro Gly Pro Val Gln Gln Ala Leu Gln
                  355   360   365

Ser Ala Glu Met Ser Leu Asp Glu Ile Glu Gln Val Ile Leu Val Gly
                  370   375   380

Gly Ala Thr Arg Val Pro Arg Val Gln Glu Val Leu Leu Lys Ala Val
20 385   390   395   400

Gly Lys Glu Glu Leu Gly Lys Asn Ile Asn Ala Asp Glu Ala Ala Ala
                  405   410   415

Met Gly Ala Val Tyr Gln Ala Ala Ala Leu Ser Lys Ala Phe Lys Val
                  420   425   430

Lys Pro Phe Val Val Arg Asp Ala Val Val Tyr Pro Ile Leu Val Glu
            435   440   445

Phe Thr Arg Glu Val Glu Glu Glu Pro Gly Ile His Ser Leu Lys His
            450   455   460

5 Asn Lys Arg Val Leu Phe Ser Arg Met Gly Pro Tyr Pro Gln Arg Lys
            465   470   475   480

Val Ile Thr Phe Asn Arg Tyr Ser His Asp Phe Asn Phe His Ile Asn
                    485   490   495

Tyr Gly Asp Leu Gly Phe Leu Gly Pro Glu Asp Leu Arg Val Phe Gly
10   500   505   510

Ser Gln Asn Leu Thr Thr Val Lys Leu Lys Gly Val Gly Asp Ser Phe
            515   520   525

Lys Lys Tyr Pro Asp Tyr Glu Ser Lys Gly Ile Lys Ala His Phe Asn
            530   535   540

15 Leu Asp Glu Ser Gly Val Leu Ser Leu Asp Arg Val Glu Ser Val Phe
    545   550   555   560

Glu Thr Leu Val Glu Asp Ser Ala Glu Glu Glu Ser Thr Leu Thr Lys
                    565   570   575

Leu Gly Asn Thr Ile Ser Ser Leu Phe Gly Gly Gly Thr Thr Pro Asp
20   580   585   590

Ala Lys Glu Asn Gly Thr Asp Thr Val Gln Glu Glu Glu Glu Ser Pro
            595   600   605

Ala Glu Gly Ser Lys Asp Glu Pro Gly Glu Gln Val Glu Leu Lys Glu
            610   615   620

```
        Glu Ala Glu Ala Pro Val Glu Asp Gly Ser Gln Pro Pro Pro Pro Glu
        625                 630             635                 640

        Pro Lys Gly Asp Ala Thr Pro Glu Gly Glu Lys Ala Thr Glu Lys Glu
                        645             650             655

  5    Asn Gly Asp Lys Ser Glu Ala Gln Lys Pro Ser Glu Lys Ala Glu Ala
                    660             665             670

        Gly Pro Glu Gly Val Ala Pro Ala Pro Glu Gly Glu Lys Lys Gln Lys
                    675             680             685

        Pro Ala Arg Lys Arg Arg Met Val Glu Glu Ile Gly Val Glu Leu Val
 10         690             695             700

        Val Leu Asp Leu Pro Asp Leu Pro Glu Asp Lys Leu Ala Gln Ser Val
        705             710             715             720

        Gln Lys Leu Gln Asp Leu Thr Leu Arg Asp Leu Glu Lys Gln Glu Arg
                        725             730             735

 15    Glu Lys Ala Ala Asn Ser Leu Glu Ala Phe Ile Phe Glu Thr Gln Asp
                        740             745             750

        Lys Leu Tyr Gln Pro Glu Tyr Gln Glu Val Ser Thr Glu Glu Gln Arg
                        755             760             765

        Glu Glu Ile Ser Gly Lys Leu Ser Ala Ala Ser Thr Trp Leu Glu Asp
 20         770             775             780

        Glu Gly Val Gly Ala Thr Thr Val Met Leu Lys Glu Lys Leu Ala Glu
        785             790             795             800

        Leu Arg Lys Leu Cys Gln Gly Leu Phe Phe Arg Val Glu Glu Arg Lys
                        805             810             815
```

Lys Trp Pro Glu Arg Leu Ser Ala Leu Asp Asn Leu Leu Asn His Ser
820 825 830

Ser Met Phe Leu Lys Gly Ala Arg Leu Ile Pro Glu Met Asp Gln Ile
835 840 845

5 Phe Thr Glu Val Glu Met Thr Thr Leu Glu Lys Val Ile Asn Glu Thr
850 855 860

Trp Ala Trp Lys Asn Ala Thr Leu Ala Glu Gln Ala Lys Leu Pro Ala
865 870 875 880

Thr Glu Lys Pro Val Leu Leu Ser Lys Asp Ile Glu Ala Lys Met Met
10 885 890 895

Ala Leu Asp Arg Glu Val Gln Tyr Leu Leu Asn Lys Ala Lys Phe Thr
900 905 910

Lys Pro Arg Pro Arg Pro Lys Asp Lys Asn Gly Thr Arg Ala Glu Pro
915 920 925

15 Pro Leu Asn Ala Ser Ala Ser Asp Gln Gly Glu Lys Val Ile Pro Pro
930 935 940

Ala Gly Gln Thr Glu Asp Ala Glu Pro Ile Ser Glu Pro Glu Lys Val
945 950 955 960

Glu Thr Gly Ser Glu Pro Gly Asp Thr Glu Pro Leu Glu Leu Gly Gly
20 965 970 975

Pro Gly Ala Glu Pro Glu Gln Lys Glu Gln Ser Thr Gly Gln Lys Arg
980 985 990

Pro Leu Lys Asn Asp Glu Leu
995

<210> 86

<211> 271

5   <212> PRT

<213> Homo sapiens

<220>

<221> Peroxiredoxin 4

<222> (1)..(271)

10   <223> Accession No. as of 29 August 2003: Q13162

<400> 86

Met Glu Ala Leu Pro Leu Leu Ala Ala Thr Thr Pro Asp His Gly Arg

1   5   10   15

15   His Arg Arg Leu Leu Leu Leu Pro Leu Leu Leu Phe Leu Leu Pro Ala

                20   25   30

Gly Ala Val Gln Gly Trp Glu Thr Glu Glu Arg Pro Arg Thr Arg Glu

            35   40   45

Glu Glu Cys His Phe Tyr Ala Gly Gly Gln Val Tyr Pro Gly Glu Ala

20   50   55   60

Ser Arg Val Ser Val Ala Asp His Ser Leu His Leu Ser Lys Ala Lys

65   70   75   80

Ile Ser Lys Pro Ala Pro Tyr Trp Glu Gly Thr Ala Val Ile Asp Gly

                85   90   95

Glu Phe Lys Glu Leu Lys Leu Thr Asp Tyr Arg Gly Lys Tyr Leu Val

             100   105   110

Phe Phe Phe Tyr Pro Leu Asp Phe Thr Phe Val Cys Pro Thr Glu Ile

             115   120   125

5   Ile Ala Phe Gly Asp Arg Leu Glu Glu Phe Arg Ser Ile Asn Thr Glu

             130   135   140

Val Val Ala Cys Ser Val Asp Ser Gln Phe Thr His Leu Ala Trp Ile

145   150   155   160

Asn Thr Pro Arg Arg Gln Gly Gly Leu Gly Pro Ile Arg Ile Pro Leu

10   165   170   175

Leu Ser Asp Leu Thr His Gln Ile Ser Lys Asp Tyr Gly Val Tyr Leu

             180   185   190

Glu Asp Ser Gly His Thr Leu Arg Gly Leu Phe Ile Ile Asp Asp Lys

             195   200   205

15 Gly Ile Leu Arg Gln Ile Thr Leu Asn Asp Leu Pro Val Gly Arg Ser

             210   215   220

Val Asp Glu Thr Leu Arg Leu Val Gln Ala Phe Gln Tyr Thr Asp Lys

225   230   235   240

His Gly Glu Val Cys Pro Ala Gly Trp Lys Pro Gly Ser Glu Thr Ile

20   245   250   255

Ile Pro Asp Pro Ala Gly Lys Leu Lys Tyr Phe Asp Lys Leu Asn

             260   265   270

```
       <210>   87

       <211>   288

       <212>   PRT

       <213>   Homo sapiens

   5   <220>

       <221>   MAWD binding protein

       <222>   (1)..(288)

       <223>   Accession No. as of 29 August 2003: P30039

       <400>   87

  10
```

```
       Met Lys Leu Pro Ile Phe Ile Ala Asp Ala Phe Thr Ala Arg Ala Phe
       1               5                   10                  15

       Arg Gly Asn Pro Ala Ala Val Cys Leu Leu Glu Asn Glu Leu Asp Glu
                       20                  25                  30

  15   Asp Met His Gln Lys Ile Ala Arg Glu Met Asn Leu Ser Glu Thr Ala
                       35                  40                  45

       Phe Ile Arg Lys Leu His Pro Thr Asp Asn Phe Ala Gln Ser Ser Cys
               50                  55                  60

       Phe Gly Leu Arg Trp Phe Thr Pro Ala Ser Glu Val Pro Leu Cys Gly
  20   65                  70                  75                  80

       His Ala Thr Leu Ala Ser Ala Ala Val Leu Phe His Lys Ile Lys Asn
                       85                  90                  95

       Met Asn Ser Thr Leu Thr Phe Val Thr Leu Ser Gly Glu Leu Arg Ala
                       100                 105                 110
```

Arg Arg Ala Glu Asp Gly Ile Val Leu Asp Leu Pro Leu Tyr Pro Ala

          115   120   125

His Pro Gln Asp Phe His Glu Val Glu Asp Leu Ile Lys Thr Ala Ile

          130   135   140

5   Gly Asn Thr Leu Val Gln Asp Ile Cys Tyr Ser Pro Asp Thr Gln Lys

          145   150   155   160

Leu Leu Val Arg Leu Ser Asp Val Tyr Asn Arg Ser Phe Leu Glu Asn

                165   170   175

Leu Lys Val Asn Thr Glu Asn Leu Leu Gln Val Glu Asn Thr Gly Lys

10   180   185   190

Val Lys Gly Leu Ile Leu Thr Leu Lys Gly Glu Pro Gly Gly Gln Thr

          195   200   205

Gln Ala Phe Asp Phe Tyr Ser Arg Tyr Phe Ala Pro Trp Val Gly Val

          210   215   220

15   Ala Glu Asp Pro Val Thr Gly Ser Ala His Ala Val Leu Ser Ser Tyr

     225   230   235   240

Trp Ser Gln His Leu Gly Lys Lys Glu Met His Ala Phe Gln Cys Ser

                245   250   255

His Arg Gly Gly Glu Leu Gly Ile Ser Leu Arg Pro Asp Gly Arg Val

20   260   265   270

Asp Ile Arg Gly Gly Ala Ala Val Val Leu Glu Gly Thr Leu Thr Ala

          275   280   285

<210> 88

<211> 511

<212> PRT

<213> Homo sapiens

5 <220>

<221> Alpha-amylase 2B precursor

<222> (1)..(511)

<223> Accession No. as of 29 August 2003: P19961

<400> 88

10

Met Lys Phe Phe Leu Leu Leu Phe Thr Ile Gly Phe Cys Trp Ala Gln

1   5   10   15

Tyr Ser Pro Asn Thr Gln Gln Gly Arg Thr Ser Ile Val His Leu Phe

                20   25   30

15 Glu Trp Arg Trp Val Asp Ile Ala Leu Glu Cys Glu Arg Tyr Leu Ala

                35   40   45

Pro Lys Gly Phe Gly Gly Val Gln Val Ser Pro Pro Asn Glu Asn Val

            50   55   60

Ala Ile His Asn Pro Phe Arg Pro Trp Trp Glu Arg Tyr Gln Pro Val

20 65   70   75   80

Ser Tyr Lys Leu Cys Thr Arg Ser Gly Asn Glu Asp Glu Phe Arg Asn

                85   90   95

Met Val Thr Arg Cys Asn Asn Val Gly Val Arg Ile Tyr Val Asp Ala

                100   105   110

Val Ile Asn His Met Ser Gly Asn Ala Val Ser Ala Gly Thr Ser Ser
        115   120   125

Thr Cys Gly Ser Tyr Phe Asn Pro Gly Ser Arg Asp Phe Pro Ala Val
        130   135   140

5   Pro Tyr Ser Gly Trp Asp Phe Asn Asp Gly Lys Cys Lys Thr Gly Ser
        145   150   155   160

Gly Asp Ile Glu Asn Tyr Asn Asp Ala Thr Gln Val Arg Asp Cys Arg
                165   170   175

Leu Val Gly Leu Leu Asp Leu Ala Leu Glu Lys Asp Tyr Val Arg Ser
10   180   185   190

Lys Ile Ala Glu Tyr Met Asn His Leu Ile Asp Ile Gly Val Ala Gly
            195   200   205

Phe Arg Leu Asp Ala Ser Lys His Met Trp Pro Gly Asp Ile Lys Ala
            210   215   220

15 Ile Leu Asp Lys Leu His Asn Leu Asn Ser Asn Trp Phe Pro Ala Gly
    225   230   235   240

Ser Lys Pro Phe Ile Tyr Gln Glu Val Ile Asp Leu Gly Gly Glu Pro
                245   250   255

Ile Lys Ser Ser Asp Tyr Phe Gly Asn Gly Arg Val Thr Glu Phe Lys
20   260   265   270

Tyr Gly Ala Lys Leu Gly Thr Val Ile Arg Lys Trp Asn Gly Glu Lys
            275   280   285

Met Ser Tyr Leu Lys Asn Trp Gly Glu Gly Trp Gly Phe Met Pro Ser
            290   295   300

Asp Arg Ala Leu Val Phe Val Asp Asn His Asp Asn Gln Arg Gly His
305   310   315   320

Gly Ala Gly Gly Ala Ser Ile Leu Thr Phe Trp Asp Ala Arg Leu Tyr
                      325   330   335

5   Lys Met Ala Val Gly Phe Met Leu Ala His Pro Tyr Gly Phe Thr Arg
                      340   345   350

    Val Met Ser Ser Tyr Arg Trp Pro Arg Gln Phe Gln Asn Gly Asn Asp
                      355   360   365

    Val Asn Asp Trp Val Gly Pro Pro Asn Asn Asn Gly Val Ile Lys Glu
10   370   375   380

    Val Thr Ile Asn Pro Asp Thr Thr Cys Gly Asn Asp Trp Val Cys Glu
    385   390   395   400

    His Arg Trp Arg Gln Ile Arg Asn Met Val Asn Phe Arg Asn Val Val
                      405   410   415

15 Asp Gly Gln Pro Phe Thr Asn Trp Tyr Asp Asn Gly Ser Asn Gln Val
                      420   425   430

    Ala Phe Gly Arg Gly Asn Arg Gly Phe Ile Val Phe Asn Asn Asp Asp
                      435   440   445

    Trp Thr Phe Ser Leu Thr Leu Gln Thr Gly Leu Pro Ala Gly Thr Tyr
20   450   455   460

    Cys Asp Val Ile Ser Gly Asp Lys Ile Asn Gly Asn Cys Thr Gly Ile
    465   470   475   480

    Lys Ile Tyr Val Ser Asp Asp Gly Lys Ala His Phe Ser Ile Ser Asn
                      485   490   495

Ser Ala Glu Asp Pro Phe Ile Ala Ile His Ala Glu Ser Lys Leu

            500   505   510

5   <210> 89

     <211> 511

     <212> PRT

     <213> Homo sapiens

     <220>

10   <221> Alpha-amylase, pancreatic precursor

     <222> (1)..(511)

     <223> Accession No. as of 29 August 2003: P04746

     <400> 89

15   Met Lys Phe Phe Leu Leu Leu Phe Thr Ile Gly Phe Cys Trp Ala Gln

     1   5   10   15

     Tyr Ser Pro Asn Thr Gln Gln Gly Arg Thr Ser Ile Val His Leu Phe

                     20   25   30

     Glu Trp Arg Trp Val Asp Ile Ala Leu Glu Cys Glu Arg Tyr Leu Ala

20   35   40   45

     Pro Lys Gly Phe Gly Gly Val Gln Val Ser Pro Pro Asn Glu Asn Val

             50   55   60

     Ala Ile Tyr Asn Pro Phe Arg Pro Trp Trp Glu Arg Tyr Gln Pro Val

     65   70   75   80

```
          Ser Tyr Lys Leu Cys Thr Arg Ser Gly Asn Glu Asp Glu Phe Arg Asn
                       85                  90                  95

          Met Val Thr Arg Cys Asn Asn Val Gly Val Arg Ile Tyr Val Asp Ala
                      100                 105                 110

      5   Val Ile Asn His Met Cys Gly Asn Ala Val Ser Ala Gly Thr Ser Ser
                      115                 120                 125

          Thr Cys Gly Ser Tyr Phe Asn Pro Gly Ser Arg Asp Phe Pro Ala Val
                      130                 135                 140

          Pro Tyr Ser Gly Trp Asp Phe Asn Asp Gly Lys Cys Lys Thr Gly Ser
     10   145                 150                 155                 160

          Gly Asp Ile Glu Asn Tyr Asn Asp Ala Thr Gln Val Arg Asp Cys Arg
                      165                 170                 175

          Leu Thr Gly Leu Leu Asp Leu Ala Leu Glu Lys Asp Tyr Val Arg Ser
                      180                 185                 190

     15   Lys Ile Ala Glu Tyr Met Asn His Leu Ile Asp Ile Gly Val Ala Gly
                      195                 200                 205

          Phe Arg Leu Asp Ala Ser Lys His Met Trp Pro Gly Asp Ile Lys Ala
                      210                 215                 220

          Ile Leu Asp Lys Leu His Asn Leu Asn Ser Asn Trp Phe Pro Ala Gly
     20   225                 230                 235                 240

          Ser Lys Pro Phe Ile Tyr Gln Glu Val Ile Asp Leu Gly Gly Glu Pro
                      245                 250                 255

          Ile Lys Ser Ser Asp Tyr Phe Gly Asn Gly Arg Val Thr Glu Phe Lys
                      260                 265                 270
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Tyr Gly Ala Lys Leu Gly Thr Val Ile Arg Lys Trp Asn Gly Glu Lys
                    275   280   285

Met Ser Tyr Leu Lys Asn Trp Gly Glu Gly Trp Gly Phe Val Pro Ser
                    290   295   300

5 Asp Arg Ala Leu Val Phe Val Asp Asn His Asp Asn Gln Arg Gly His
        305   310   315   320

Gly Ala Gly Gly Ala Ser Ile Leu Thr Phe Trp Asp Ala Arg Leu Tyr
                        325   330   335

Lys Met Ala Val Gly Phe Met Leu Ala His Pro Tyr Gly Phe Thr Arg
10   340   345   350

Val Met Ser Ser Tyr Arg Trp Pro Arg Gln Phe Gln Asn Gly Asn Asp
                        355   360   365

Val Asn Asp Trp Val Gly Pro Pro Asn Asn Asn Gly Val Ile Lys Glu
                        370   375   380

15 Val Thr Ile Asn Pro Asp Thr Thr Cys Gly Asn Asp Trp Val Cys Glu
        385   390   395   400

His Arg Trp Arg Gln Ile Arg Asn Met Val Ile Phe Arg Asn Val Val
                        405   410   415

Asp Gly Gln Pro Phe Thr Asn Trp Tyr Asp Asn Gly Ser Asn Gln Val
20   420   425   430

Ala Phe Gly Arg Gly Asn Arg Gly Phe Ile Val Phe Asn Asn Asp Asp
                        435   440   445

Trp Ser Phe Ser Leu Thr Leu Gln Thr Gly Leu Pro Ala Gly Thr Tyr
                        450   455   460

Cys Asp Val Ile Ser Gly Asp Lys Ile Asn Gly Asn Cys Thr Gly Ile

465   470   475   480

Lys Ile Tyr Val Ser Asp Asp Gly Lys Ala His Phe Ser Ile Ser Asn

             485   490   495

5   Ser Ala Glu Asp Pro Phe Ile Ala Ile His Ala Glu Ser Lys Leu

             500   505   510

<210> 90

10   <211> 553

<212> PRT

<213> Homo sapiens

<220>

<221> ATP synthase alpha chain

15   <222> (1)..(553)

<223> Accession No. as of 29 August 2003: P25705

<400> 90

Met Leu Ser Val Arg Val Ala Ala Ala Val Val Arg Ala Leu Pro Arg

20   1   5   10   15

Arg Ala Gly Leu Val Ser Arg Asn Ala Leu Gly Ser Ser Phe Ile Ala

             20   25   30

Ala Arg Asn Phe His Ala Ser Asn Thr His Leu Gln Lys Thr Gly Thr

             35   40   45

Ala Glu Met Ser Ser Ile Leu Glu Glu Arg Ile Leu Gly Ala Asp Thr

         50   55   60

Ser Val Asp Leu Glu Glu Thr Gly Arg Val Leu Ser Ile Gly Asp Gly

65   70   75   80

5   Ile Ala Arg Val His Gly Leu Arg Asn Val Gln Ala Glu Glu Met Val

                      85   90   95

Glu Phe Ser Ser Gly Leu Lys Gly Met Ser Leu Asn Leu Glu Pro Asp

                  100   105   110

Asn Val Gly Val Val Val Phe Gly Asn Asp Lys Leu Ile Lys Glu Gly

10   115   120   125

Asp Ile Val Lys Arg Thr Gly Ala Ile Val Asp Val Pro Val Gly Glu

         130   135   140

Glu Leu Leu Gly Arg Val Val Asp Ala Leu Gly Asn Ala Ile Asp Gly

145   150   155   160

15 Lys Gly Pro Ile Gly Ser Lys Thr Arg Arg Arg Val Gly Leu Lys Ala

                  165   170   175

Pro Gly Ile Ile Pro Arg Ile Ser Val Arg Glu Pro Met Gln Thr Gly

                  180   185   190

Ile Lys Ala Val Asp Ser Leu Val Pro Ile Gly Arg Gly Gln Arg Glu

20   195   200   205

Leu Ile Ile Gly Asp Arg Gln Thr Gly Lys Thr Ser Ile Ala Ile Asp

         210   215   220

Thr Ile Ile Asn Gln Lys Arg Phe Asn Asp Gly Ser Asp Glu Lys Lys

225   230   235   240

Lys Leu Tyr Cys Ile Tyr Val Ala Ile Gly Gln Lys Arg Ser Thr Val
                    245   250   255

Ala Gln Leu Val Lys Arg Leu Thr Asp Ala Asp Ala Met Lys Tyr Thr
                    260   265   270

5   Ile Val Val Ser Ala Thr Ala Ser Asp Ala Ala Pro Leu Gln Tyr Leu
                    275   280   285

Ala Pro Tyr Ser Gly Cys Ser Met Gly Glu Tyr Phe Arg Asp Asn Gly
                290   295   300

Lys His Ala Leu Ile Ile Tyr Asp Asp Leu Ser Lys Gln Ala Val Ala
10 305   310   315   320

Tyr Arg Gln Met Ser Leu Leu Leu Arg Arg Pro Pro Gly Arg Glu Ala
                    325   330   335

Tyr Pro Gly Asp Val Phe Tyr Leu His Ser Arg Leu Leu Glu Arg Ala
                    340   345   350

15 Ala Lys Met Asn Asp Ala Phe Gly Gly Gly Ser Leu Thr Ala Leu Pro
                    355   360   365

Val Ile Glu Thr Gln Ala Gly Asp Val Ser Ala Tyr Ile Pro Thr Asn
                    370   375   380

Val Ile Ser Ile Thr Asp Gly Gln Ile Phe Leu Glu Thr Glu Leu Phe
20 385   390   395   400

Tyr Lys Gly Ile Arg Pro Ala Ile Asn Val Gly Leu Ser Val Ser Arg
                    405   410   415

Val Gly Ser Ala Ala Gln Thr Arg Ala Met Lys Gln Val Ala Gly Thr
                    420   425   430

Met Lys Leu Glu Leu Ala Gln Tyr Arg Glu Val Ala Ala Phe Ala Gln

            435   440   445

    Phe Gly Ser Asp Leu Asp Ala Ala Thr Gln Gln Leu Leu Ser Arg Gly

            450   455   460

5   Val Arg Leu Thr Glu Leu Leu Lys Gln Gly Gln Tyr Ser Pro Met Ala

        465   470   475   480

    Ile Glu Glu Gln Val Ala Val Ile Tyr Ala Gly Val Arg Gly Tyr Leu

                    485   490   495

    Asp Lys Leu Glu Pro Ser Lys Ile Thr Lys Phe Glu Asn Ala Phe Leu

10   500   505   510

    Ser His Val Val Ser Gln His Gln Ala Leu Leu Gly Thr Ile Arg Ala

            515   520   525

    Asp Gly Lys Ile Ser Glu Gln Ser Asp Ala Lys Leu Lys Glu Ile Val

        530   535   540

15 Thr Asn Phe Leu Ala Gly Phe Glu Ala

    545   550

    <210>   91

20 <211>   742

    <212>   PRT

    <213>   Homo sapiens

    <220>

    <221>   Bile-salt-activated lipase precursor

<222>   (1)..(742)

<223>   Accession No. as of 29 August 2003: P19835

<400>   91

5   Met Gly Arg Leu Gln Leu Val Val Leu Gly Leu Thr Cys Cys Trp Ala
    1   5   10   15

    Val Ala Ser Ala Ala Lys Leu Gly Ala Val Tyr Thr Glu Gly Gly Phe
                    20   25   30

    Val Glu Gly Val Asn Lys Lys Leu Gly Leu Leu Gly Asp Ser Val Asp
10   35   40   45

    Ile Phe Lys Gly Ile Pro Phe Ala Ala Pro Thr Lys Ala Leu Glu Asn
                50   55   60

    Pro Gln Pro His Pro Gly Trp Gln Gly Thr Leu Lys Ala Lys Asn Phe
    65   70   75   80

15 Lys Lys Arg Cys Leu Gln Ala Thr Ile Thr Gln Asp Ser Thr Tyr Gly
                    85   90   95

    Asp Glu Asp Cys Leu Tyr Leu Asn Ile Trp Val Pro Gln Gly Arg Lys
                    100   105   110

    Gln Val Ser Arg Asp Leu Pro Val Met Ile Trp Ile Tyr Gly Gly Ala
20   115   120   125

    Phe Leu Met Gly Ser Gly His Gly Ala Asn Phe Leu Asn Asn Tyr Leu
                130   135   140

    Tyr Asp Gly Glu Glu Ile Ala Thr Arg Gly Asn Val Ile Val Val Thr
    145   150   155   160

Phe Asn Tyr Arg Val Gly Pro Leu Gly Phe Leu Ser Thr Gly Asp Ala
            165   170   175

Asn Leu Pro Gly Asn Tyr Gly Leu Arg Asp Gln His Met Ala Ile Ala
            180   185   190

5 Trp Val Lys Arg Asn Ile Ala Ala Phe Gly Gly Asp Pro Asn Asn Ile
            195   200   205

Thr Leu Phe Gly Glu Ser Ala Gly Gly Ala Ser Val Ser Leu Gln Thr
            210   215   220

Leu Ser Pro Tyr Asn Lys Gly Leu Ile Arg Arg Ala Ile Ser Gln Ser
10 225   230   235   240

Gly Val Ala Leu Ser Pro Trp Val Ile Gln Lys Asn Pro Leu Phe Trp
            245   250   255

Ala Lys Lys Val Ala Glu Lys Val Gly Cys Pro Val Gly Asp Ala Ala
            260   265   270

15 Arg Met Ala Gln Cys Leu Lys Val Thr Asp Pro Arg Ala Leu Thr Leu
            275   280   285

Ala Tyr Lys Val Pro Leu Ala Gly Leu Glu Tyr Pro Met Leu His Tyr
            290   295   300

Val Gly Phe Val Pro Val Ile Asp Gly Asp Phe Ile Pro Ala Asp Pro
20 305   310   315   320

Ile Asn Leu Tyr Ala Asn Ala Ala Asp Ile Asp Tyr Ile Ala Gly Thr
            325   330   335

Asn Asn Met Asp Gly His Ile Phe Ala Ser Ile Asp Met Pro Ala Ile
            340   345   350

Asn Lys Gly Asn Lys Lys Val Thr Glu Glu Asp Phe Tyr Lys Leu Val

      355   360   365

Ser Glu Phe Thr Ile Thr Lys Gly Leu Arg Gly Ala Lys Thr Thr Phe

      370   375   380

5 Asp Val Tyr Thr Glu Ser Trp Ala Gln Asp Pro Ser Gln Glu Asn Lys

      385   390   395   400

Lys Lys Thr Val Val Asp Phe Glu Thr Asp Val Leu Phe Leu Val Pro

              405   410   415

Thr Glu Ile Ala Leu Ala Gln His Arg Ala Asn Ala Lys Ser Ala Lys

10   420   425   430

Thr Tyr Ala Tyr Leu Phe Ser His Pro Ser Arg Met Pro Val Tyr Pro

          435   440   445

Lys Trp Val Gly Ala Asp His Ala Asp Asp Ile Gln Tyr Val Phe Gly

      450   455   460

15 Lys Pro Phe Ala Thr Pro Thr Gly Tyr Arg Pro Gln Asp Arg Thr Val

      465   470   475   480

Ser Lys Ala Met Ile Ala Tyr Trp Thr Asn Phe Ala Lys Thr Gly Asp

              485   490   495

Pro Asn Met Gly Asp Ser Ala Val Pro Thr His Trp Glu Pro Tyr Thr

20   500   505   510

Thr Glu Asn Ser Gly Tyr Leu Glu Ile Thr Lys Lys Met Gly Ser Ser

      515   520   525

Ser Met Lys Arg Ser Leu Arg Thr Asn Phe Leu Arg Tyr Trp Thr Leu

      530   535   540

Thr Tyr Leu Ala Leu Pro Thr Val Thr Asp Gln Glu Ala Thr Pro Val
545   550   555   560

Pro Pro Thr Gly Asp Ser Glu Ala Thr Pro Val Pro Pro Thr Gly Asp
                    565   570   575

5   Ser Glu Thr Ala Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro
                         580   585   590

Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly
             595   600   605

Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro
10   610   615   620

Pro Val Pro Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr
625   630   635   640

Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly Ala
                 645   650   655

15   Pro Pro Val Pro Pro Thr Gly Asp Ala Gly Pro Pro Val Pro Pro
             660   665   670

Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser Gly
         675   680   685

Ala Pro Pro Val Thr Pro Thr Gly Asp Ser Glu Thr Ala Pro Val Pro
20   690   695   700

Pro Thr Gly Asp Ser Gly Ala Pro Pro Val Pro Pro Thr Gly Asp Ser
705   710   715   720

Glu Ala Ala Pro Val Pro Pro Thr Asp Asp Ser Lys Glu Ala Gln Met
                 725   730   735

Pro Ala Val Ile Arg Phe

740

5   <210>   92

     <211>   467

     <212>   PRT

     <213>   Homo sapiens

     <220>

10   <221>   Pancreatic lipase related protein precursor

     <222>   (1)..(467)

     <223>   Accession No. as of 29 August 2003: P54315

     <400>   92

15   Met Leu Ile Phe Trp Thr Ile Thr Leu Phe Leu Leu Gly Ala Ala Lys
     1   5   10   15

     Gly Lys Glu Val Cys Tyr Glu Asp Leu Gly Cys Phe Ser Asp Thr Glu
                     20   25   30

     Pro Trp Gly Gly Thr Ala Ile Arg Pro Leu Lys Ile Leu Pro Trp Ser
20   35   40   45

     Pro Glu Lys Ile Gly Thr Arg Phe Leu Leu Tyr Thr Asn Glu Asn Pro
                 50   55   60

     Asn Asn Phe Gln Ile Leu Leu Leu Ser Asp Pro Ser Thr Ile Glu Ala
     65   70   75   80

Ser Asn Phe Gln Met Asp Arg Lys Thr Arg Phe Ile Ile His Gly Phe

                85   90   95

Ile Asp Lys Gly Asp Glu Ser Trp Val Thr Asp Met Cys Lys Lys Leu

               100   105   110

5 Phe Glu Val Glu Glu Val Asn Cys Ile Cys Val Asp Trp Lys Lys Gly

               115   120   125

Ser Gln Ala Thr Tyr Thr Gln Ala Ala Asn Asn Val Arg Val Val Gly

               130   135   140

Ala Gln Val Ala Gln Met Leu Asp Ile Leu Leu Thr Glu Tyr Ser Tyr

10 145   150   155   160

Pro Pro Ser Lys Val His Leu Ile Gly His Ser Leu Gly Ala His Val

               165   170   175

Ala Gly Glu Ala Gly Ser Lys Thr Pro Gly Leu Ser Arg Ile Thr Gly

               180   185   190

15 Leu Asp Pro Val Glu Ala Ser Phe Glu Ser Thr Pro Glu Glu Val Arg

               195   200   205

Leu Asp Pro Ser Asp Ala Asp Phe Val Asp Val Ile His Thr Asp Ala

               210   215   220

Ala Pro Leu Ile Pro Phe Leu Gly Phe Gly Thr Asn Gln Gln Met Gly

20 225   230   235   240

His Leu Asp Phe Phe Pro Asn Gly Gly Glu Ser Met Pro Gly Cys Lys

               245   250   255

Lys Asn Ala Leu Ser Gln Ile Val Asp Leu Asp Gly Ile Trp Ala Gly

               260   265   270

Thr Arg Asp Phe Val Ala Cys Asn His Leu Arg Ser Tyr Lys Tyr Tyr

        275   280   285

Leu Glu Ser Ile Leu Asn Pro Asp Gly Phe Ala Ala Tyr Pro Cys Thr

        290   295   300

5 Ser Tyr Lys Ser Phe Glu Ser Asp Lys Cys Phe Pro Cys Pro Asp Gln

   305   310   315   320

Gly Cys Pro Gln Met Gly His Tyr Ala Asp Lys Phe Ala Gly Arg Thr

            325   330   335

Ser Glu Glu Gln Gln Lys Phe Phe Leu Asn Thr Gly Glu Ala Ser Asn

10   340   345   350

Phe Ala Arg Trp Arg Tyr Gly Val Ser Ile Thr Leu Ser Gly Arg Thr

        355   360   365

Ala Thr Gly Gln Ile Lys Val Ala Leu Phe Gly Asn Lys Gly Asn Thr

        370   375   380

15 His Gln Tyr Ser Ile Phe Arg Gly Ile Leu Lys Pro Gly Ser Thr His

   385   390   395   400

Ser Tyr Glu Phe Asp Ala Lys Leu Asp Val Gly Thr Ile Glu Lys Val

            405   410   415

Lys Phe Leu Trp Asn Asn Asn Val Ile Asn Pro Thr Leu Pro Lys Val

20   420   425   430

Gly Ala Thr Lys Ile Thr Val Gln Lys Gly Glu Glu Lys Thr Val Tyr

        435   440   445

Asn Phe Cys Ser Glu Asp Thr Val Arg Glu Asp Thr Leu Leu Thr Leu

        450   455   460

Thr Pro Cys

465

5   <210>   93

     <211>   469

     <212>   PRT

     <213>   Homo sapiens

     <220>

10   <221>   Pancreatic lipase related protein 2 precursor

     <222>   (1)..(469)

     <223>   Accession No. as of 29 August 2003: P54317

     <400>   93

15   Met Leu Pro Pro Trp Thr Leu Gly Leu Leu Leu Ala Thr Val Arg
     1   5   10   15

     Gly Lys Glu Val Cys Tyr Gly Gln Leu Gly Cys Phe Ser Asp Glu Lys
                     20   25   30

     Pro Trp Ala Gly Thr Leu Gln Arg Pro Val Lys Leu Leu Pro Trp Ser
20   35   40   45

     Pro Glu Asp Ile Asp Thr Arg Phe Leu Leu Tyr Thr Asn Glu Asn Pro
                     50   55   60

     Asn Asn Phe Gln Leu Ile Thr Gly Thr Glu Pro Asp Thr Ile Glu Ala
     65   70   75   80

```
    Ser Asn Phe Gln Leu Asp Arg Lys Thr Arg Phe Ile Ile His Gly Phe
                    85                  90                  95

    Leu Asp Lys Ala Glu Asp Ser Trp Pro Ser Asp Met Cys Lys Lys Met
                    100                 105                 110

 5  Phe Glu Val Glu Lys Val Asn Cys Ile Cys Val Asp Trp Arg His Gly
                    115                 120                 125

    Ser Arg Ala Met Tyr Thr Gln Ala Val Gln Asn Ile Arg Val Val Gly
                    130                 135                 140

    Ala Glu Thr Ala Phe Leu Ile Gln Ala Leu Ser Thr Gln Leu Gly Tyr
10  145                 150                 155                 160

    Ser Leu Glu Asp Val His Val Ile Gly His Ser Leu Gly Ala His Thr
                    165                 170                 175

    Ala Ala Glu Ala Gly Arg Arg Leu Gly Gly Arg Val Gly Arg Ile Thr
                    180                 185                 190

15  Gly Leu Asp Pro Ala Gly Pro Cys Phe Gln Asp Glu Pro Glu Glu Val
                    195                 200                 205

    Arg Leu Asp Pro Ser Asp Ala Val Phe Val Asp Val Ile His Thr Asp
                    210                 215                 220

    Ser Ser Pro Ile Val Pro Ser Leu Gly Phe Gly Met Ser Gln Lys Val
20  225                 230                 235                 240

    Gly His Leu Asp Phe Phe Pro Asn Gly Gly Lys Glu Met Pro Gly Cys
                    245                 250                 255

    Lys Lys Asn Val Leu Ser Thr Ile Thr Asp Ile Asp Gly Ile Trp Glu
                    260                 265                 270
```

Gly Ile Gly Gly Phe Val Ser Cys Asn His Leu Arg Ser Phe Glu Tyr

          275   280   285

    Tyr Ser Ser Ser Val Leu Asn Pro Asp Gly Phe Leu Gly Tyr Pro Cys

              290   295   300

5   Ala Ser Tyr Asp Glu Phe Gln Glu Ser Lys Cys Phe Pro Cys Pro Ala

        305   310   315   320

    Glu Gly Cys Pro Lys Met Gly His Tyr Ala Asp Gln Phe Lys Gly Lys

                      325   330   335

    Thr Ser Ala Val Glu Gln Thr Phe Phe Leu Asn Thr Gly Glu Ser Gly

10   340   345   350

    Asn Phe Thr Ser Trp Arg Tyr Lys Val Ser Val Thr Leu Ser Gly Lys

                  355   360   365

    Glu Lys Val Asn Gly Tyr Ile Arg Ile Ala Leu Tyr Gly Ser Asn Glu

              370   375   380

15 Asn Ser Lys Gln Tyr Glu Ile Phe Lys Gly Ser Leu Lys Pro Asp Ala

        385   390   395   400

    Ser His Thr Cys Ala Ile Asp Val Asp Phe Asn Val Gly Lys Ile Gln

                  405   410   415

    Lys Val Lys Phe Leu Trp Asn Lys Arg Gly Ile Asn Leu Ser Glu Pro

20   420   425   430

    Lys Leu Gly Ala Ser Gln Ile Thr Val Gln Ser Gly Glu Asp Gly Thr

              435   440   445

    Glu Tyr Asn Phe Cys Ser Ser Asp Thr Val Glu Glu Asn Val Leu Gln

          450   455   460

Ser Leu Tyr Pro Cys

465

5   <210>   94

    <211>   465

    <212>   PRT

    <213>   Homo sapiens

    <220>

10 <221>   Triacylglycerol lipase, pancreatic precursor

    <222>   (1)..(465)

    <223>   Accession No. as of 29 August 2003: P16233

    <400>   94

15 Met Leu Pro Leu Trp Thr Leu Ser Leu Leu Leu Gly Ala Val Ala Gly

    1   5   10   15

    Lys Glu Val Cys Tyr Glu Arg Leu Gly Cys Phe Ser Asp Asp Ser Pro

                    20   25   30

    Trp Ser Gly Ile Thr Glu Arg Pro Leu His Ile Leu Pro Trp Ser Pro

20   35   40   45

    Lys Asp Val Asn Thr Arg Phe Leu Leu Tyr Thr Asn Glu Asn Pro Asn

                50   55   60

    Asn Phe Gln Glu Val Ala Ala Asp Ser Ser Ser Ile Ser Gly Ser Asn

    65   70   75   80

Phe Lys Thr Asn Arg Lys Thr Arg Phe Ile Ile His Gly Phe Ile Asp

                85   90   95

Lys Gly Glu Glu Asn Trp Leu Ala Asn Val Cys Lys Asn Leu Phe Lys

               100   105   110

5   Val Glu Ser Val Asn Cys Ile Cys Val Asp Trp Lys Gly Gly Ser Arg

               115   120   125

Thr Gly Tyr Thr Gln Ala Ser Gln Asn Ile Arg Ile Val Gly Ala Glu

               130   135   140

Val Ala Tyr Phe Val Glu Phe Leu Gln Ser Ala Phe Gly Tyr Ser Pro

10 145   150   155   160

Ser Asn Val His Val Ile Gly His Ser Leu Gly Ala His Ala Ala Gly

               165   170   175

Glu Ala Gly Arg Arg Thr Asn Gly Thr Ile Gly Arg Ile Thr Gly Leu

               180   185   190

15 Asp Pro Ala Glu Pro Cys Phe Gln Gly Thr Pro Glu Leu Val Arg Leu

               195   200   205

Asp Pro Ser Asp Ala Lys Phe Val Asp Val Ile His Thr Asp Gly Ala

               210   215   220

Pro Ile Val Pro Asn Leu Gly Phe Gly Met Ser Gln Val Val Gly His

20 225   230   235   240

Leu Asp Phe Phe Pro Asn Gly Gly Val Glu Met Pro Gly Cys Lys Lys

               245   250   255

Asn Ile Leu Ser Gln Ile Val Asp Ile Asp Gly Ile Trp Glu Gly Thr

               260   265   270

Arg Asp Phe Ala Ala Cys Asn His Leu Arg Ser Tyr Lys Tyr Tyr Thr

     275   280   285

Asp Ser Ile Val Asn Pro Asp Gly Phe Ala Gly Phe Pro Cys Ala Ser

     290   295   300

5 Tyr Asn Val Phe Thr Ala Asn Lys Cys Phe Pro Cys Pro Ser Gly Gly

     305   310   315   320

Cys Pro Gln Met Gly His Tyr Ala Asp Arg Tyr Pro Gly Lys Thr Asn

            325   330   335

Asp Val Gly Gln Lys Phe Tyr Leu Asp Thr Gly Asp Ala Ser Asn Phe

10   340   345   350

Ala Arg Trp Arg Tyr Lys Val Ser Val Thr Leu Ser Gly Lys Lys Val

     355   360   365

Thr Gly His Ile Leu Val Ser Leu Phe Gly Asn Lys Gly Asn Ser Lys

     370   375   380

15 Gln Tyr Glu Ile Phe Lys Gly Thr Leu Lys Pro Asp Ser Thr His Ser

     385   390   395   400

Asn Glu Phe Asp Ser Asp Val Asp Val Gly Asp Leu Gln Met Val Lys

            405   410   415

Phe Ile Trp Tyr Asn Asn Val Ile Asn Pro Thr Leu Pro Arg Val Gly

20   420   425   430

Ala Ser Lys Ile Ile Val Glu Thr Asn Val Gly Lys Gln Phe Asn Phe

     435   440   445

Cys Ser Pro Glu Thr Val Arg Glu Glu Val Leu Leu Thr Leu Thr Pro

     450   455   460

Cys

465

5   <210>   95

     <211>   572

     <212>   PRT

     <213>   Homo sapiens

     <220>

10   <221>   Dihydropyrimidinase related protein-2

     <222>   (1)..(572)

     <223>   Accession No. as of 29 August 2003: Q16555

     <400>   95

15   Met Ser Tyr Gln Gly Lys Lys Asn Ile Pro Arg Ile Thr Ser Asp Arg
     1   5   10   15

     Leu Leu Ile Lys Gly Gly Lys Ile Val Asn Asp Asp Gln Ser Phe Tyr
                     20   25   30

     Ala Asp Ile Tyr Met Glu Asp Gly Leu Ile Lys Gln Ile Gly Glu Asn
20   35   40   45

     Leu Ile Val Pro Gly Gly Val Lys Thr Ile Glu Ala His Ser Arg Met
                 50   55   60

     Val Ile Pro Gly Gly Ile Asp Val His Thr Arg Phe Gln Met Pro Asp
     65   70   75   80

Gln Gly Met Thr Ser Ala Asp Asp Phe Phe Gln Gly Thr Lys Ala Ala
                85   90   95

Leu Ala Gly Gly Thr Thr Met Ile Ile Asp His Val Val Pro Glu Pro
                100   105   110

5 Gly Thr Ser Leu Leu Ala Ala Phe Asp Gln Trp Arg Glu Trp Ala Asp
                115   120   125

Ser Lys Ser Cys Cys Asp Tyr Ser Leu His Val Asp Ile Ser Glu Trp
        130   135   140

His Lys Gly Ile Gln Glu Glu Met Glu Ala Leu Val Lys Asp His Gly
10 145   150   155   160

Val Asn Ser Phe Leu Val Tyr Met Ala Phe Lys Asp Arg Phe Gln Leu
                165   170   175

Thr Asp Cys Gln Ile Tyr Glu Val Leu Ser Val Ile Arg Asp Ile Gly
                180   185   190

15 Ala Ile Ala Gln Val His Ala Glu Asn Gly Asp Ile Ile Ala Glu Glu
            195   200   205

Gln Gln Arg Ile Leu Asp Leu Gly Ile Thr Gly Pro Glu Gly His Val
        210   215   220

Leu Ser Arg Pro Glu Glu Val Glu Ala Glu Ala Val Asn Arg Ala Ile
20 225   230   235   240

Thr Ile Ala Asn Gln Thr Asn Cys Pro Leu Tyr Ile Thr Lys Val Met
            245   250   255

Ser Lys Ser Ser Ala Glu Val Ile Ala Gln Ala Arg Lys Lys Gly Thr
            260   265   270

Val Val Tyr Gly Glu Pro Ile Thr Ala Ser Leu Gly Thr Asp Gly Ser

　　　275　　　　　　　　　　280　　　　　　　　　　285

His Tyr Trp Ser Lys Asn Trp Ala Lys Ala Ala Ala Phe Val Thr Ser

　　　290　　　　　　　　　　295　　　　　　　　　　300

5　　Pro Pro Leu Ser Pro Asp Pro Thr Thr Pro Asp Phe Leu Asn Ser Leu

　　　305　　　　　　　　　　310　　　　　　　　　　315　　　　　　　　　　320

Leu Ser Cys Gly Asp Leu Gln Val Thr Gly Ser Ala His Cys Thr Phe

　　　　　　　　　　325　　　　　　　　　　330　　　　　　　　　　335

Asn Thr Ala Gln Lys Ala Val Gly Lys Asp Asn Phe Thr Leu Ile Pro

10　　　　　　　　340　　　　　　　　　　345　　　　　　　　　　350

Glu Gly Thr Asn Gly Thr Glu Glu Arg Met Ser Val Ile Trp Asp Lys

　　　　　　　　355　　　　　　　　　　360　　　　　　　　　　365

Ala Val Val Thr Gly Lys Met Asp Glu Asn Gln Phe Val Ala Val Thr

　　　　　　　　370　　　　　　　　　　375　　　　　　　　　　380

15　　Ser Thr Asn Ala Ala Lys Val Phe Asn Leu Tyr Pro Arg Lys Gly Arg

　　　385　　　　　　　　　　390　　　　　　　　　　395　　　　　　　　　　400

Ile Ala Val Gly Ser Asp Ala Asp Leu Val Ile Trp Asp Pro Asp Ser

　　　　　　　　　　405　　　　　　　　　　410　　　　　　　　　　415

Val Lys Thr Ile Ser Ala Lys Thr His Asn Ser Ser Leu Glu Tyr Asn

20　　　　　　　　420　　　　　　　　　　425　　　　　　　　　　430

Ile Phe Glu Gly Met Glu Cys Arg Gly Ser Pro Leu Val Val Ile Ser

　　　　　　　435　　　　　　　　　　440　　　　　　　　　　445

Gln Gly Lys Ile Val Leu Glu Asp Gly Thr Leu His Val Thr Glu Gly

　　　450　　　　　　　　　　455　　　　　　　　　　460

Ser Gly Arg Tyr Ile Pro Arg Lys Pro Phe Pro Asp Phe Val Tyr Lys

465   470   475   480

Arg Ile Lys Ala Arg Ser Arg Leu Ala Glu Leu Arg Gly Val Pro Arg

                485   490   495

5   Gly Leu Tyr Asp Gly Pro Val Cys Glu Val Ser Val Thr Pro Lys Thr

                500   505   510

Val Thr Pro Ala Ser Ser Ala Lys Thr Ser Pro Ala Lys Gln Gln Ala

            515   520   525

Pro Pro Val Arg Asn Leu His Gln Ser Gly Phe Ser Leu Ser Gly Ala

10   530   535   540

Gln Ile Asp Asp Asn Ile Pro Arg Arg Thr Thr Gln Arg Ile Val Ala

545   550   555   560

Pro Pro Gly Gly Arg Ala Asn Ile Thr Ser Leu Gly

            565   570

15

<210> 96

<211> 500

<212> PRT

20 <213> Homo sapiens

<220>

<221> 4-aminobutyrate aminotransferase, mitochondrial precursor

<222> (1)..(500)

<223> Accession No. as of 29 August 2003: P80404

<400> 96

Met Ala Ser Met Leu Leu Ala Gln Arg Leu Ala Cys Ser Phe Gln His

1   5   10   15

5 Thr Tyr Arg Leu Leu Val Pro Gly Ser Arg His Ile Ser Gln Ala Ala

            20   25   30

Ala Lys Val Asp Val Glu Phe Asp Tyr Asp Gly Pro Leu Met Lys Thr

        35   40   45

Glu Val Pro Gly Pro Arg Ser Gln Glu Leu Met Lys Gln Leu Asn Ile

10   50   55   60

Ile Gln Asn Ala Glu Ala Val His Phe Phe Cys Asn Tyr Glu Glu Ser

65   70   75   80

Arg Gly Asn Tyr Leu Val Asp Val Asp Gly Asn Arg Met Leu Asp Leu

                85   90   95

15 Tyr Ser Gln Ile Ser Ser Val Pro Ile Gly Tyr Ser Asp Pro Ala Leu

                100   105   110

Val Lys Leu Ile Gln Gln Pro Gln Asn Ala Ser Met Phe Val Asn Arg

        115   120   125

Pro Ala Leu Glu Ile Leu Pro Pro Glu Asn Phe Val Glu Lys Leu Arg

20   130   135   140

Gln Ser Leu Leu Ser Val Ala Pro Lys Gly Met Ser Gln Leu Ile Thr

145   150   155   160

Met Ala Cys Gly Ser Cys Ser Asn Glu Asn Ala Leu Lys Thr Ile Phe

                165   170   175

Met Trp Tyr Arg Ser Lys Glu Arg Gly Gln Arg Gly Phe Ser Lys Glu
          180   185   190

Glu Leu Glu Thr Cys Met Ile Asn Gln Ala Pro Trp Cys Pro Asp Tyr
          195   200   205

5 Ser Ile Leu Ser Phe Met Gly Ser Phe His Gly Arg Thr Met Gly Cys
          210   215   220

Leu Ala Thr Thr His Ser Lys Ala Ile His Lys Ile Asp Ile Pro Ser
225   230   235   240

Phe Asp Trp Pro Ile Ala Pro Phe Pro Arg Leu Lys Tyr Pro Leu Glu
10   245   250   255

Glu Phe Val Lys Glu Asn Gln Gln Glu Glu Ala Gly Cys Leu Glu Glu
          260   265   270

Val Glu Asp Leu Ile Val Lys Tyr Arg Lys Lys Lys Thr Val Ala
          275   280   285

15 Gly Ile Ile Val Glu Pro Ile Gln Ser Glu Gly Gly Asp Asn His Ala
          290   295   300

Ser Asp Asp Phe Phe Arg Lys Leu Arg Asp Ile Ala Arg Lys His Cys
305   310   315   320

Cys Ala Phe Leu Val Asp Glu Val Gln Thr Gly Gly Gly Cys Thr Gly
20   325   330   335

Lys Phe Trp Ala His Glu His Trp Gly Leu Asp Asp Pro Ala Asp Val
          340   345   350

Met Thr Phe Ser Lys Lys Met Met Thr Gly Gly Phe Phe Leu Lys Glu
          355   360   365

Glu Phe Arg Pro Asn Ala Pro Tyr Arg Ile Phe Asn Thr Trp Leu Gly

     370   375   380

Asp Pro Ser Lys Asn Leu Leu Leu Ala Glu Val Ile Asn Ile Ile Lys

     385   390   395   400

5   Arg Glu Asp Leu Leu Asn Asn Ala Ala His Ala Gly Lys Ala Leu Leu

                      405   410   415

Thr Gly Leu Leu Asp Leu Gln Ala Arg Tyr Pro Gln Phe Ile Ser Arg

                 420   425   430

Val Arg Gly Arg Gly Thr Phe Cys Ser Phe Asp Thr Pro Asp Asp Ser

10   435   440   445

Ile Arg Asn Lys Leu Ile Leu Ile Ala Arg Asn Lys Gly Val Val Leu

             450   455   460

Gly Gly Cys Gly Asp Lys Ser Ile Arg Phe Arg Pro Thr Leu Val Phe

     465   470   475   480

15   Arg Asp His His Ala His Leu Phe Leu Asn Ile Phe Ser Asp Ile Leu

                 485   490   495

Ala Asp Phe Lys

             500

20

    <210> 97

    <211> 423

    <212> PRT

    <213> Homo sapiens

<220>

<221>   Glycine amidiontransferase, mitochondrial precursor

<222>   (1)..(423)

<223>   Accession No. as of 29 August 2003: P50440

5   <400>   97

     Met Leu Arg Val Arg Cys Leu Arg Gly Gly Ser Arg Gly Ala Glu Ala
     1   5   10   15

     Val His Tyr Ile Gly Ser Arg Leu Gly Arg Thr Leu Thr Gly Trp Val
10   20   25   30

     Gln Arg Thr Phe Gln Ser Thr Gln Ala Ala Thr Ala Ser Ser Arg Asn
                     35   40   45

     Ser Cys Ala Ala Asp Asp Lys Ala Thr Glu Pro Leu Pro Lys Asp Cys
                 50   55   60

15   Pro Val Ser Ser Tyr Asn Glu Trp Asp Pro Leu Glu Glu Val Ile Val
     65   70   75   80

     Gly Arg Ala Glu Asn Ala Cys Val Pro Pro Phe Thr Ile Glu Val Lys
                     85   90   95

     Ala Asn Thr Tyr Glu Lys Tyr Trp Pro Phe Tyr Gln Lys Gln Gly Gly
20   100   105   110

     His Tyr Phe Pro Lys Asp His Leu Lys Lys Ala Val Ala Glu Ile Glu
                     115   120   125

     Glu Met Cys Asn Ile Leu Lys Thr Glu Gly Val Thr Val Arg Arg Pro
                 130   135   140

Asp Pro Ile Asp Trp Ser Leu Lys Tyr Lys Thr Pro Asp Phe Glu Ser

145   150   155   160

Thr Gly Leu Tyr Ser Ala Met Pro Arg Asp Ile Leu Ile Val Val Gly

                    165   170   175

5   Asn Glu Ile Ile Glu Ala Pro Met Ala Trp Arg Ser Arg Phe Phe Glu

                    180   185   190

Tyr Arg Ala Tyr Arg Ser Ile Ile Lys Asp Tyr Phe His Arg Gly Ala

            195   200   205

Lys Trp Thr Thr Ala Pro Lys Pro Thr Met Ala Asp Glu Leu Tyr Asn

10   210   215   220

Gln Asp Tyr Pro Ile His Ser Val Glu Asp Arg His Lys Leu Ala Ala

225   230   235   240

Gln Gly Lys Phe Val Thr Thr Glu Phe Glu Pro Cys Phe Asp Ala Ala

                    245   250   255

15   Asp Phe Ile Arg Ala Gly Arg Asp Ile Phe Ala Gln Arg Ser Gln Val

                    260   265   270

Thr Asn Tyr Leu Gly Ile Glu Trp Met Arg Arg His Leu Ala Pro Asp

            275   280   285

Tyr Arg Val His Ile Ile Ser Phe Lys Asp Pro Asn Pro Met His Ile

20   290   295   300

Asp Ala Thr Phe Asn Ile Ile Gly Pro Gly Ile Val Leu Ser Asn Pro

305   310   315   320

Asp Arg Pro Cys His Gln Ile Asp Leu Phe Lys Lys Ala Gly Trp Thr

                    325   330   335

Ile Ile Thr Pro Pro Thr Pro Ile Ile Pro Asp Asp His Pro Leu Trp

340   345   350

Met Ser Ser Lys Trp Leu Ser Met Asn Val Leu Met Leu Asp Glu Lys

355   360   365

5 Arg Val Met Val Asp Ala Asn Glu Val Pro Ile Gln Lys Met Phe Glu

370   375   380

Lys Leu Gly Ile Thr Thr Ile Lys Val Asn Ile Arg Asn Ala Asn Ser

385   390   395   400

Leu Gly Gly Gly Phe His Cys Trp Thr Cys Asp Val Arg Arg Arg Gly

10   405   410   415

Thr Leu Gln Ser Tyr Leu Asp

420

15 <210> 98

<211> 654

<212> PRT

<213> Homo sapiens

<220>

20 <221> GRP 78

<222> (1)..(654)

<223> Accession No. as of 29 August 2003: P11021

<220>

<221> misc_feature

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        <222>   (302)..(302)

        <223>   Xaa can be any naturally occurring amino acid

        <220>

        <221>   misc_feature

  5     <222>   (329)..(329)

        <223>   Xaa can be any naturally occurring amino acid

        <220>

        <221>   misc_feature

        <222>   (344)..(344)

 10     <223>   Xaa can be any naturally occurring amino acid

        <220>

        <221>   misc_feature

        <222>   (461)..(461)

        <223>   Xaa can be any naturally occurring amino acid

 15     <400>   98
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```
        Met Lys Leu Ser Leu Val Ala Ala Met Leu Leu Leu Leu Ser Ala

        1                 5                   10                  15

        Ala Arg Ala Lys Glu Glu Asp Met Gly Thr Val Val Ala Ile His Leu

 20                       20                  25                  30

        Gly Thr Thr Tyr Pro Cys Val Gly Val Phe Lys Asn Gly Arg Met Glu

                          35                  40                  45

        Ile Ile Ala Asn Asp Gln Gly Asn Arg Ile Met Pro Ser Tyr Val Ala

                          50                  55                  60
```

```
         Phe Thr Pro Glu Gly Glu Cys Leu Ile Gly Asp Ala Ala Lys Asn Gln

             65                  70              75                  80

         Leu Thr Ser Asn Pro Lys Asn Thr Val Phe Asp Ala Lys Arg Leu Ile

                         85                  90              95

  5  Gly Arg Arg Trp His Asp Pro Ser Val Gln Gln Asp Ile Glu Phe Leu

                     100                 105                 110

         Pro Phe Lys Val Val Glu Lys Asn Thr Lys Ser Tyr Ile Gln Ile Asp

                     115                 120                 125

         Val Gly Gly Gly Gln Thr Lys Thr Phe Ala Pro Lys Glu Ile Ser Ala

 10          130                 135                 140

         Met Val Leu Thr Lys Met Lys Glu Asn Ala Glu Ala Tyr Leu Gly Lys

             145                 150                 155                 160

         Val Thr His Ala Val Val Thr Ala Pro Ala Tyr Phe Asn Asp Ala Gln

                         165                 170                 175

 15  Cys Gln Ala Thr Lys Asp Ala Gly Thr Ile Ala Asp Leu Asn Val Met

                     180                 185                 190

         Arg Ile Ile Asn Lys Pro Thr Ala Ala Ala Ile Ala Tyr Gly Leu Asp

                     195                 200                 205

         Lys Arg Glu Gly Glu Lys Asn Ile Leu Val Phe Asp Leu Gly Gly Gly

 20          210                 215                 220

         Thr Phe Asp Val Ser Leu Leu Thr Ile Asp Asn Gly Val Phe Lys Val

             225                 230                 235                 240

         Val Ala Thr Asn Gly Asp Thr Tyr Leu Gly Gly Glu Asp Phe Asp Gln

                     245                 250                 255
```

Arg Val Met Glu His Phe Ile Lys Leu Tyr Lys Lys Lys Thr Gly Lys

260   265   270

Asp Val Arg Lys Asp Asn Arg Ala Val Gln Lys Leu Trp Arg Lys Val

275   280   285

5   Glu Lys Ala Lys Arg Ala Leu Ser Ser Gln His Gln Ala Xaa Val Ile

290   295   300

Glu Ile Glu Ser Phe Tyr Glu Gly Glu Asp Phe Ser Glu Thr Leu Thr

305   310   315   320

Gln Ala Lys Phe Glu Glu Leu Asn Xaa Asp Leu Phe Gln Ser Thr Met

10   325   330   335

Lys Pro Ser Gln Arg Ser Val Xaa Lys Val Leu Glu Asp Ser Asp Leu

340   345   350

Lys Lys Ser Asp Ile Asp Glu Thr Val Leu Val Gly Gly Phe Thr Gln

355   360   365

15   Ile Pro Lys Ile Gln Gln Leu Val Lys Glu Phe Phe Asn Gly Lys Glu

370   375   380

Leu Ser Arg Gly Ile Ser Pro Tyr Glu Ala Val Ala Tyr Gly Ala Ala

385   390   395   400

Val Gln Ala Gly Val Leu Ser Gly Asp Gln Asp Thr Gly Asp Leu Val

20   405   410   415

Leu Leu Asp Ile Cys Pro Leu Thr Leu Gly Ile Glu Thr Val Gly Gly

420   425   430

Val Met Thr Lys Leu Ile Pro Arg Asn Thr Val Val Pro Thr Lys Lys

435   440   445

Ser Gln Ile Phe Ser Thr Ala Phe Asp Asn Gln Pro Xaa Thr Ile Lys

         450   455   460

Val Tyr Glu Gly Lys Gln Pro Leu Thr Lys Asp Asn His Leu Leu Gly

         465   470   475   480

5   Thr Phe Asp Leu Thr Gly Ile Pro Pro Ala Pro Cys Gly Val Pro Gln

                 485   490   495

Ile Glu Val Thr Phe Glu Met Asp Val Ser Asp Ile Leu Gln Val Thr

             500   505   510

Ala Lys Asp Lys Gly Thr Arg Tyr Lys Asn Lys Ile Thr Ile Thr Asn

10   515   520   525

Asp Gln Asn His Leu Thr Pro Glu Asp Ile Glu Arg Met Val Asn Asp

         530   535   540

Ala Glu Lys Phe Ala Glu Glu Asp Lys Lys Leu Lys Glu Cys Thr Asp

545   550   555   560

15   Thr Arg Asn Glu Leu Glu Ser Tyr Ala Tyr Ser Leu Lys Asn Gln Ile

                 565   570   575

Gly Asp Lys Glu Lys Leu Gly Gly Lys Leu Ser Ser Glu Asp Lys Glu

             580   585   590

Thr Met Glu Lys Thr Val Glu Glu Lys Thr Glu Trp Leu Glu Ser His

20   595   600   605

Gln Asp Ala Asp Thr Glu Asp Phe Lys Ala Lys Lys Lys Glu Leu Glu

         610   615   620

Glu Ile Val Gln Pro Ile Ile Ser Lys Leu Tyr Gly Ser Ala Gly Pro

625   630   635   640

Pro Pro Thr Gly Glu Glu Asp Thr Ala Glu Lys Asp Glu Leu

                   645   650

5   <210> 99

    <211> 325

    <212> PRT

    <213> Homo sapiens

    <220>

10 <221> Eukaryotic translation initiation factor 3 subunit 2

    <222> (1)..(325)

    <223> Accession No. as of 29 August 2003: Q13347

    <400> 99

15 Met Lys Pro Ile Leu Leu Gln Gly His Glu Arg Ser Ile Thr Gln Ile

    1   5   10   15

    Lys Tyr Asn Arg Glu Gly Asp Leu Leu Phe Thr Val Ala Lys Asp Pro

                   20   25   30

    Ile Val Asn Val Trp Tyr Ser Val Asn Gly Glu Arg Leu Gly Thr Tyr

20   35   40   45

    Met Gly His Thr Gly Ala Val Trp Cys Val Asp Ala Asp Trp Asp Thr

               50   55   60

    Lys His Val Leu Thr Gly Ser Ala Asp Asn Ser Cys Arg Leu Trp Asp

    65   70   75   80

Cys Glu Thr Gly Lys Gln Leu Ala Leu Leu Lys Thr Asn Ser Ala Val

                    85   90   95

Arg Thr Cys Gly Phe Asp Phe Gly Gly Asn Ile Ile Met Phe Ser Thr

                    100   105   110

5   Asp Lys Gln Met Gly Tyr Gln Cys Phe Val Ser Phe Phe Asp Leu Arg

                    115   120   125

    Asp Pro Ser Gln Ile Asp Asn Asn Glu Pro Tyr Met Lys Ile Pro Cys

                    130   135   140

    Asn Asp Ser Lys Ile Thr Ser Ala Val Trp Gly Pro Leu Gly Glu Cys

10 145   150   155   160

    Ile Ile Ala Gly His Glu Ser Gly Glu Leu Asn Gln Tyr Ser Ala Lys

                    165   170   175

    Ser Gly Glu Val Leu Val Asn Val Lys Glu His Ser Arg Gln Ile Asn

                    180   185   190

15 Asp Ile Gln Leu Ser Arg Asp Met Thr Met Phe Val Thr Ala Ser Lys

                    195   200   205

    Asp Asn Thr Ala Lys Leu Phe Asp Ser Thr Thr Leu Glu His Gln Lys

                    210   215   220

    Thr Phe Arg Thr Glu Arg Pro Val Asn Ser Ala Ala Leu Ser Pro Asn

20 225   230   235   240

    Tyr Asp His Val Val Leu Gly Gly Gly Gln Glu Ala Met Asp Val Thr

                    245   250   255

    Thr Thr Ser Thr Arg Ile Gly Lys Phe Glu Ala Arg Phe Phe His Leu

                    260   265   270

Ala Phe Glu Glu Glu Phe Gly Arg Val Lys Gly His Phe Gly Pro Ile

    275   280   285

Asn Ser Val Ala Phe His Pro Asp Gly Lys Ser Tyr Ser Ser Gly Gly

    290   295   300

5   Glu Asp Gly Tyr Val Arg Ile His Tyr Phe Asp Pro Gln Tyr Phe Glu

    305   310   315   320

Phe Glu Phe Glu Ala

    325

10

    <210>   100

    <211>   572

    <212>   PRT

    <213>   Homo sapiens

15 <220>

    <221>   Dihydropyrimidinase related protein-2

    <222>   (1)..(572)

    <223>   Accession No. as of 29 August 2003: Q16555

    <400>   100

20

Met Ser Tyr Gln Gly Lys Lys Asn Ile Pro Arg Ile Thr Ser Asp Arg

1   5   10   15

Leu Leu Ile Lys Gly Gly Lys Ile Val Asn Asp Asp Gln Ser Phe Tyr

        20   25   30

```
      Ala Asp Ile Tyr Met Glu Asp Gly Leu Ile Lys Gln Ile Gly Glu Asn

              35                  40                  45

      Leu Ile Val Pro Gly Gly Val Lys Thr Ile Glu Ala His Ser Arg Met

              50                  55                  60

  5   Val Ile Pro Gly Gly Ile Asp Val His Thr Arg Phe Gln Met Pro Asp

              65                  70                  75                  80

      Gln Gly Met Thr Ser Ala Asp Asp Phe Phe Gln Gly Thr Lys Ala Ala

                      85                  90                  95

      Leu Ala Gly Gly Thr Thr Met Ile Ile Asp His Val Val Pro Glu Pro

 10                   100                 105                 110

      Gly Thr Ser Leu Leu Ala Ala Phe Asp Gln Trp Arg Glu Trp Ala Asp

                      115                 120                 125

      Ser Lys Ser Cys Cys Asp Tyr Ser Leu His Val Asp Ile Ser Glu Trp

                      130                 135                 140

 15   His Lys Gly Ile Gln Glu Glu Met Glu Ala Leu Val Lys Asp His Gly

      145                 150                 155                 160

      Val Asn Ser Phe Leu Val Tyr Met Ala Phe Lys Asp Arg Phe Gln Leu

                      165                 170                 175

      Thr Asp Cys Gln Ile Tyr Glu Val Leu Ser Val Ile Arg Asp Ile Gly

 20                   180                 185                 190

      Ala Ile Ala Gln Val His Ala Glu Asn Gly Asp Ile Ile Ala Glu Glu

                      195                 200                 205

      Gln Gln Arg Ile Leu Asp Leu Gly Ile Thr Gly Pro Glu Gly His Val

                      210                 215                 220
```

Leu Ser Arg Pro Glu Glu Val Glu Ala Glu Ala Val Asn Arg Ala Ile

225   230   235   240

Thr Ile Ala Asn Gln Thr Asn Cys Pro Leu Tyr Ile Thr Lys Val Met

                    245   250   255

5   Ser Lys Ser Ser Ala Glu Val Ile Ala Gln Ala Arg Lys Lys Gly Thr

                    260   265   270

Val Val Tyr Gly Glu Pro Ile Thr Ala Ser Leu Gly Thr Asp Gly Ser

            275   280   285

His Tyr Trp Ser Lys Asn Trp Ala Lys Ala Ala Ala Phe Val Thr Ser

10   290   295   300

Pro Pro Leu Ser Pro Asp Pro Thr Thr Pro Asp Phe Leu Asn Ser Leu

305   310   315   320

Leu Ser Cys Gly Asp Leu Gln Val Thr Gly Ser Ala His Cys Thr Phe

                    325   330   335

15 Asn Thr Ala Gln Lys Ala Val Gly Lys Asp Asn Phe Thr Leu Ile Pro

                    340   345   350

Glu Gly Thr Asn Gly Thr Glu Glu Arg Met Ser Val Ile Trp Asp Lys

            355   360   365

Ala Val Val Thr Gly Lys Met Asp Glu Asn Gln Phe Val Ala Val Thr

20   370   375   380

Ser Thr Asn Ala Ala Lys Val Phe Asn Leu Tyr Pro Arg Lys Gly Arg

385   390   395   400

Ile Ala Val Gly Ser Asp Ala Asp Leu Val Ile Trp Asp Pro Asp Ser

            405   410   415

```
      Val Lys Thr Ile Ser Ala Lys Thr His Asn Ser Ser Leu Glu Tyr Asn

               420                 425                 430

      Ile Phe Glu Gly Met Glu Cys Arg Gly Ser Pro Leu Val Val Ile Ser

               435                 440                 445

  5   Gln Gly Lys Ile Val Leu Glu Asp Gly Thr Leu His Val Thr Glu Gly

               450                 455                 460

      Ser Gly Arg Tyr Ile Pro Arg Lys Pro Phe Pro Asp Phe Val Tyr Lys

               465                 470                 475                 480

      Arg Ile Lys Ala Arg Ser Arg Leu Ala Glu Leu Arg Gly Val Pro Arg

 10                    485                 490                 495

      Gly Leu Tyr Asp Gly Pro Val Cys Glu Val Ser Val Thr Pro Lys Thr

               500                 505                 510

      Val Thr Pro Ala Ser Ser Ala Lys Thr Ser Pro Ala Lys Gln Gln Ala

               515                 520                 525

 15   Pro Pro Val Arg Asn Leu His Gln Ser Gly Phe Ser Leu Ser Gly Ala

               530                 535                 540

      Gln Ile Asp Asp Asn Ile Pro Arg Arg Thr Thr Gln Arg Ile Val Ala

      545                 550                 555                 560

      Pro Pro Gly Gly Arg Ala Asn Ile Thr Ser Leu Gly

 20                    565                 570
```

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      <210>  101

      <211>  561
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<212>   PRT

<213>   Homo sapiens

<220>

<221>   Phosphoglucomutase (EC 5.4.2.2) (Glucose phosphomutase) (PGM)

<222>   (1)..(561)

<223>   Accession No. as of 29 August 2003: P36871

<400>   101

Val Lys Ile Val Thr Val Lys Thr Gln Ala Tyr Gln Asp Gln Lys Pro
1   5   10   15

Gly Thr Ser Gly Leu Arg Lys Arg Val Lys Val Phe Gln Ser Ser Ala
                20   25   30

Asn Tyr Ala Glu Asn Phe Ile Gln Ser Ile Ile Ser Thr Val Glu Pro
                35   40   45

Ala Gln Arg Gln Glu Ala Thr Leu Val Val Gly Gly Asp Gly Arg Phe
        50   55   60

Tyr Met Lys Glu Ala Ile Gln Leu Ile Ala Arg Ile Ala Ala Ala Asn
65   70   75   80

Gly Ile Gly Arg Leu Val Ile Gly Gln Asn Gly Ile Leu Ser Thr Pro
                85   90   95

Ala Val Ser Cys Ile Ile Arg Lys Ile Lys Ala Ile Gly Gly Ile Ile
            100   105   110

Leu Thr Ala Ser His Asn Pro Gly Gly Pro Asn Gly Asp Phe Gly Ile
        115   120   125

Lys Phe Asn Ile Ser Asn Gly Gly Pro Ala Pro Glu Ala Ile Thr Asp
    130   135   140

Lys Ile Phe Gln Ile Ser Lys Thr Ile Glu Glu Tyr Ala Val Cys Pro
145   150   155   160

5   Asp Leu Lys Val Asp Leu Gly Val Leu Gly Lys Gln Gln Phe Asp Leu
                165   170   175

Glu Asn Lys Phe Lys Pro Phe Thr Val Glu Ile Val Asp Ser Val Glu
            180   185   190

Ala Tyr Ala Thr Met Leu Arg Ser Ile Phe Asp Phe Ser Ala Leu Lys
10   195   200   205

Glu Leu Leu Ser Gly Pro Asn Arg Leu Lys Ile Arg Ile Asp Ala Met
            210   215   220

His Gly Val Val Gly Pro Tyr Val Lys Lys Ile Leu Cys Glu Glu Leu
225   230   235   240

15 Gly Ala Pro Ala Asn Ser Ala Val Asn Cys Val Pro Leu Glu Asp Phe
                245   250   255

Gly Gly His His Pro Asp Pro Asn Leu Thr Tyr Ala Ala Asp Leu Val
            260   265   270

Glu Thr Met Lys Ser Gly Glu His Asp Phe Gly Ala Ala Phe Asp Gly
20   275   280   285

Asp Gly Asp Arg Asn Met Ile Leu Gly Lys His Gly Phe Phe Val Asn
            290   295   300

Pro Ser Asp Ser Val Ala Val Ile Ala Ala Asn Ile Phe Ser Ile Pro
305   310   315   320

Tyr Phe Gln Gln Thr Gly Val Arg Gly Phe Ala Arg Ser Met Pro Thr

                325   330   335

Ser Gly Ala Leu Asp Arg Val Ala Ser Ala Thr Lys Ile Ala Leu Tyr

                340   345   350

5   Glu Thr Pro Thr Gly Trp Lys Phe Phe Gly Asn Leu Met Asp Ala Ser

            355   360   365

Lys Leu Ser Leu Cys Gly Glu Glu Ser Phe Gly Thr Gly Ser Asp His

            370   375   380

Ile Arg Glu Lys Asp Gly Leu Trp Ala Val Leu Ala Trp Leu Ser Ile

10   385   390   395   400

Leu Ala Thr Arg Lys Gln Ser Val Glu Asp Ile Leu Lys Asp His Trp

                405   410   415

Gln Lys Tyr Gly Arg Asn Phe Phe Thr Arg Tyr Asp Tyr Glu Glu Val

                420   425   430

15   Glu Ala Glu Gly Ala Asn Lys Met Met Lys Asp Leu Glu Ala Leu Met

            435   440   445

Phe Asp Arg Ser Phe Val Gly Lys Gln Phe Ser Ala Asn Asp Lys Val

            450   455   460

Tyr Thr Val Glu Lys Ala Asp Asn Phe Glu Tyr Ser Asp Pro Val Asp

20   465   470   475   480

Gly Ser Ile Ser Arg Asn Gln Gly Leu Arg Leu Ile Phe Thr Asp Gly

            485   490   495

Ser Arg Ile Val Phe Arg Leu Ser Gly Thr Gly Ser Ala Gly Ala Thr

            500   505   510

Ile Arg Leu Tyr Ile Asp Ser Tyr Glu Lys Asp Val Ala Lys Ile Asn

            515   520   525

Gln Asp Pro Gln Val Met Leu Ala Pro Leu Ile Ser Ile Ala Leu Lys

            530   535   540

5   Val Ser Gln Leu Gln Glu Arg Thr Gly Arg Thr Ala Pro Thr Val Ile

    545   550   555   560

    Thr

10

    <210>   102

    <211>   263

    <212>   PRT

    <213>   Homo sapiens

15 <220>

    <221>   Proteasome subunit alpha type 1

    <222>   (1)..(263)

    <223>   Accession No. as of 29 August 2003: P25786

    <400>   102

20

    Met Phe Arg Asn Gln Tyr Asp Asn Asp Val Thr Val Trp Ser Pro Gln

    1   5   10   15

    Gly Arg Ile His Gln Ile Glu Tyr Ala Met Glu Ala Val Lys Gln Gly

            20   25   30

Ser Ala Thr Val Gly Leu Lys Ser Lys Thr His Ala Val Leu Val Ala
         35   40   45

Leu Lys Arg Ala Gln Ser Glu Leu Ala Ala His Gln Lys Lys Ile Leu
         50   55   60

5   His Val Asp Asn His Ile Gly Ile Ser Ile Ala Gly Leu Thr Ala Asp
         65   70   75   80

Ala Arg Leu Leu Cys Asn Phe Met Arg Gln Glu Cys Leu Asp Ser Arg
                  85   90   95

Phe Val Phe Asp Arg Pro Leu Pro Val Ser Arg Leu Val Ser Leu Ile
10   100   105   110

Gly Ser Lys Thr Gln Ile Pro Thr Gln Arg Tyr Gly Arg Arg Pro Tyr
                 115   120   125

Gly Val Gly Leu Leu Ile Ala Gly Tyr Asp Asp Met Gly Pro His Ile
                 130   135   140

15 Phe Gln Thr Cys Pro Ser Ala Asn Tyr Phe Asp Cys Arg Ala Met Ser
    145   150   155   160

Ile Gly Ala Arg Ser Gln Ser Ala Arg Thr Tyr Leu Glu Arg His Met
                 165   170   175

Ser Glu Phe Met Glu Cys Asn Leu Asn Glu Leu Val Lys His Gly Leu
20   180   185   190

Arg Ala Leu Arg Glu Thr Leu Pro Ala Glu Gln Asp Leu Thr Thr Lys
                 195   200   205

Asn Val Ser Ile Gly Ile Val Gly Lys Asp Leu Glu Phe Thr Ile Tyr
                 210   215   220

```
        Asp Asp Asp Asp Val Ser Pro Phe Leu Glu Gly Leu Glu Glu Arg Pro

        225                 230                 235                 240

        Gln Arg Lys Ala Gln Pro Ala Gln Pro Ala Asp Glu Pro Ala Glu Lys

                            245                 250                 255

   5    Ala Asp Glu Pro Met Glu His

                            260




        <210>   103

  10    <211>   205

        <212>   PRT

        <213>   Homo sapiens

        <220>

        <221>   Heat shock 27 kDa protein

  15    <222>   (1)..(205)

        <223>   Accession No. as of 29 August 2003: P04792

        <400>   103




        Met Thr Glu Arg Arg Val Pro Phe Ser Leu Leu Arg Gly Pro Ser Trp

  20    1                   5                   10                  15

        Asp Pro Phe Arg Asp Trp Tyr Pro His Ser Arg Leu Phe Asp Gln Ala

                            20                  25                  30

        Phe Gly Leu Pro Arg Leu Pro Glu Glu Trp Ser Gln Trp Leu Gly Gly

                            35                  40                  45
```

Ser Ser Trp Pro Gly Tyr Val Arg Pro Leu Pro Pro Ala Ala Ile Glu
          50   55   60

Ser Pro Ala Val Ala Ala Pro Ala Tyr Ser Arg Ala Leu Ser Arg Gln
          65   70   75   80

5   Leu Ser Ser Gly Val Ser Glu Ile Arg His Thr Ala Asp Arg Trp Arg
                      85   90   95

Val Ser Leu Asp Val Asn His Phe Ala Pro Asp Glu Leu Thr Val Lys
              100   105   110

Thr Lys Asp Gly Val Val Glu Ile Thr Gly Lys His Glu Glu Arg Gln
10   115   120   125

Asp Glu His Gly Tyr Ile Ser Arg Cys Phe Thr Arg Lys Tyr Thr Leu
          130   135   140

Pro Pro Gly Val Asp Pro Thr Gln Val Ser Ser Ser Leu Ser Pro Glu
145   150   155   160

15 Gly Thr Leu Thr Val Glu Ala Pro Met Pro Lys Leu Ala Thr Gln Ser
                  165   170   175

Asn Glu Ile Thr Ile Pro Val Thr Phe Glu Ser Arg Ala Gln Leu Gly
              180   185   190

Gly Pro Glu Ala Ala Lys Ser Asp Glu Thr Ala Ala Lys
20   195   200   205

          <210>   104

          <211>   868

<212>   PRT

<213>   Homo sapiens

<220>

<221>   Programmed cell death 6 interacting protein (Hp95)

5   <222>   (1)..(868)

<223>   Accession No. as of 29 August 2003: Q8WUM4

<400>   104

Met Ala Thr Phe Ile Ser Val Gln Leu Lys Lys Thr Ser Glu Val Asp

10   1   5   10   15

Leu Ala Lys Pro Leu Val Lys Phe Ile Gln Gln Thr Tyr Pro Ser Gly

                    20   25   30

Gly Glu Glu Gln Ala Gln Tyr Cys Arg Ala Ala Glu Glu Leu Ser Lys

                    35   40   45

15   Leu Arg Arg Ala Ala Val Gly Arg Pro Leu Asp Lys His Glu Gly Ala

                50   55   60

Leu Glu Thr Leu Leu Arg Tyr Tyr Asp Gln Ile Cys Ser Ile Glu Pro

65   70   75   80

Lys Phe Pro Phe Ser Glu Asn Gln Ile Cys Leu Thr Phe Thr Trp Lys

20   85   90   95

Asp Ala Phe Asp Lys Gly Ser Leu Phe Gly Gly Ser Val Lys Leu Ala

                    100   105   110

Leu Ala Ser Leu Gly Tyr Glu Lys Ser Cys Val Leu Phe Asn Cys Ala

                    115   120   125

Ala Leu Ala Ser Gln Ile Ala Ala Glu Gln Asn Leu Asp Asn Asp Glu
          130   135   140

Gly Leu Lys Ile Ala Ala Lys His Tyr Gln Phe Ala Ser Gly Ala Phe
          145   150   155   160

5   Leu His Ile Lys Glu Thr Val Leu Ser Ala Leu Ser Arg Glu Pro Thr
                    165   170   175

Val Asp Ile Ser Pro Asp Thr Val Gly Thr Leu Ser Leu Ile Met Leu
              180   185   190

Ala Gln Ala Gln Glu Val Phe Phe Leu Lys Ala Thr Arg Asp Lys Met
10   195   200   205

Lys Asp Ala Ile Ile Ala Lys Leu Ala Asn Gln Ala Ala Asp Tyr Phe
          210   215   220

Gly Asp Ala Phe Lys Gln Cys Gln Tyr Lys Asp Thr Leu Pro Lys Glu
    225   230   235   240

15 Val Phe Pro Val Leu Ala Ala Lys His Cys Ile Met Gln Ala Asn Ala
                    245   250   255

Glu Tyr His Gln Ser Ile Leu Ala Lys Gln Gln Lys Lys Phe Gly Glu
          260   265   270

Glu Ile Ala Arg Leu Gln His Ala Ala Glu Leu Ile Lys Thr Val Ala
20   275   280   285

Ser Arg Tyr Asp Glu Tyr Val Asn Val Lys Asp Phe Ser Asp Lys Ile
          290   295   300

Asn Arg Ala Leu Ala Ala Ala Lys Lys Asp Asn Asp Phe Ile Tyr His
305   310   315   320

Asp Arg Val Pro Asp Leu Lys Asp Leu Asp Pro Ile Gly Lys Ala Thr
                325   330   335

Leu Val Lys Ser Thr Pro Val Asn Val Pro Ile Ser Gln Lys Phe Thr
                340   345   350

5   Asp Leu Phe Glu Lys Met Val Pro Val Ser Val Gln Gln Ser Leu Ala
                355   360   365

Ala Tyr Asn Gln Arg Lys Ala Asp Leu Val Asn Arg Ser Ile Ala Gln
                370   375   380

Met Arg Glu Ala Thr Thr Leu Ala Asn Gly Val Leu Ala Ser Leu Asn
10 385   390   395   400

Leu Pro Ala Ala Ile Glu Asp Val Ser Gly Asp Thr Val Pro Gln Ser
                405   410   415

Ile Leu Thr Lys Ser Arg Ser Val Ile Glu Gln Gly Gly Ile Gln Thr
                420   425   430

15 Val Asp Gln Leu Ile Lys Glu Leu Pro Glu Leu Leu Gln Arg Asn Arg
                435   440   445

Glu Ile Leu Asp Glu Ser Leu Arg Leu Leu Asp Glu Glu Glu Ala Thr
                450   455   460

Asp Asn Asp Leu Arg Ala Lys Phe Lys Glu Arg Trp Gln Arg Thr Pro
20 465   470   475   480

Ser Asn Glu Leu Tyr Lys Pro Leu Arg Ala Glu Gly Thr Asn Phe Arg
                485   490   495

Thr Val Leu Asp Lys Ala Val Gln Ala Asp Gly Gln Val Lys Glu Cys
                500   505   510

Tyr Gln Ser His Arg Asp Thr Ile Val Leu Leu Cys Lys Pro Glu Pro
            515   520   525

Glu Leu Asn Ala Ala Ile Pro Ser Ala Asn Pro Ala Lys Thr Met Gln
            530   535   540

5   Gly Ser Glu Val Val Asn Val Leu Lys Ser Leu Leu Ser Asn Leu Asp
        545   550   555   560

Glu Val Lys Lys Glu Arg Glu Gly Leu Glu Asn Asp Leu Lys Ser Val
                565   570   575

Asn Phe Asp Met Thr Ser Lys Phe Leu Thr Ala Leu Ala Gln Asp Gly
10   580   585   590

Val Ile Asn Glu Glu Ala Leu Ser Val Thr Glu Leu Asp Arg Val Tyr
            595   600   605

Gly Gly Leu Thr Thr Lys Val Gln Glu Ser Leu Lys Lys Gln Glu Gly
        610   615   620

15 Leu Leu Lys Asn Ile Gln Val Ser His Gln Glu Phe Ser Lys Met Lys
        625   630   635   640

Gln Ser Asn Asn Glu Ala Asn Leu Arg Glu Glu Val Leu Lys Asn Leu
                645   650   655

Ala Thr Ala Tyr Asp Asn Phe Val Glu Leu Val Ala Asn Leu Lys Glu
20   660   665   670

Gly Thr Lys Phe Tyr Asn Glu Leu Thr Glu Ile Leu Val Arg Phe Gln
            675   680   685

Asn Lys Cys Ser Asp Ile Val Phe Ala Arg Lys Thr Glu Arg Asp Glu
        690   695   700

Leu Leu Lys Asp Leu Gln Gln Ser Ile Ala Arg Glu Pro Ser Ala Pro

705   710   715   720

Ser Ile Pro Thr Pro Ala Tyr Gln Ser Ser Pro Ala Gly Gly His Ala

725   730   735

5   Pro Thr Pro Pro Thr Pro Ala Pro Arg Thr Met Pro Pro Thr Lys Pro

740   745   750

Gln Pro Pro Ala Arg Pro Pro Pro Val Leu Pro Ala Asn Arg Ala

755   760   765

Pro Ser Ala Thr Ala Pro Ser Pro Val Gly Ala Gly Thr Ala Ala Pro

10   770   775   780

Ala Pro Ser Gln Thr Pro Gly Ser Ala Pro Pro Gln Ala Gln Gly

785   790   795   800

Pro Pro Tyr Pro Thr Tyr Pro Gly Tyr Pro Gly Tyr Cys Gln Met Pro

805   810   815

15 Met Pro Met Gly Tyr Asn Pro Tyr Ala Tyr Gly Gln Tyr Asn Met Pro

820   825   830

Tyr Pro Pro Val Tyr His Gln Ser Pro Gly Gln Ala Pro Tyr Pro Gly

835   840   845

Pro Gln Gln Pro Ser Tyr Pro Phe Pro Gln Pro Pro Gln Gln Ser Tyr

20 850   855   860

Tyr Pro Gln Gln

865

<210> 105

<211> 280

<212> PRT

<213> Homo sapiens

5   <220>

<221> Similar to four and a half LIM domains 3

<222> (1)..(280)

<223> Accession No. as of 29 August 2003: Q9BVA2

<400> 105

10

```
Met Ser Glu Ser Phe Asp Cys Ala Lys Cys Asn Glu Ser Leu Tyr Gly
1               5                   10                  15

Arg Lys Tyr Ile Gln Thr Asp Ser Gly Pro Tyr Cys Val Pro Cys Tyr
                20                  25                  30

15 Asp Asn Thr Phe Ala Asn Thr Cys Ala Glu Cys Gln Gln Leu Ile Gly
                35                  40                  45

His Asp Ser Arg Glu Leu Phe Tyr Glu Asp Arg His Phe His Glu Gly
        50                  55                  60

Cys Phe Arg Cys Cys Arg Cys Gln Arg Ser Leu Ala Asp Glu Pro Phe
20 65                  70                  75                  80

Thr Cys Gln Asp Ser Glu Leu Leu Cys Asn Asp Cys Tyr Cys Ser Ala
                85                  90                  95

Phe Ser Ser Gln Cys Ser Ala Cys Gly Glu Thr Val Met Pro Gly Ser
                100                 105                 110
```

Arg Lys Leu Glu Tyr Gly Gly Gln Thr Trp His Glu His Cys Phe Leu

115   120   125

Cys Ser Gly Cys Glu Gln Pro Leu Gly Ser Arg Ser Phe Val Pro Asp

130   135   140

5   Lys Gly Ala His Tyr Cys Val Pro Cys Tyr Glu Asn Lys Phe Ala Pro

145   150   155   160

Arg Cys Ala Arg Cys Ser Lys Thr Leu Thr Gln Gly Gly Val Thr Tyr

165   170   175

Arg Asp Gln Pro Trp His Arg Glu Cys Leu Val Cys Thr Gly Cys Gln

10   180   185   190

Thr Pro Leu Ala Gly Gln Gln Phe Thr Ser Arg Asp Glu Asp Pro Tyr

195   200   205

Cys Val Ala Cys Phe Gly Glu Leu Phe Ala Pro Lys Cys Ser Ser Cys

210   215   220

15 Lys Arg Pro Ile Val Gly Leu Gly Gly Gly Lys Tyr Val Ser Phe Glu

225   230   235   240

Asp Arg His Trp His His Asn Cys Phe Ser Cys Ala Arg Cys Ser Thr

245   250   255

Ser Leu Val Gly Gln Gly Phe Val Pro Asp Gly Asp Gln Val Leu Cys

20   260   265   270

Gln Gly Cys Ser Gln Ala Gly Pro

275   280

<210> 106

<211> 280

<212> PRT

<213> Homo sapiens

5   <220>

<221> Skeletal muscle LIM-protein 2 (SLIM 2)

<222> (1)..(280)

<223> Accession No. as of 29 August 2003: Q13643

<400> 106

10

Met Ser Glu Ser Phe Asp Cys Ala Lys Cys Asn Glu Ser Leu Tyr Gly

1   5   10   15

Arg Lys Tyr Ile Gln Thr Asp Ser Gly Pro Tyr Cys Val Pro Cys Tyr

                  20   25   30

15 Asp Asn Thr Phe Ala Asn Thr Cys Ala Glu Cys Gln Gln Leu Ile Gly

                  35   40   45

His Asp Ser Arg Glu Leu Phe Tyr Glu Asp Arg His Phe His Glu Gly

        50   55   60

Cys Phe Arg Cys Cys Arg Cys Gln Arg Ser Leu Ala Asp Glu Pro Phe

20 65   70   75   80

Thr Arg Gln Asp Ser Glu Leu Leu Cys Asn Asp Cys Tyr Cys Ser Ala

                  85   90   95

Phe Ser Ser Gln Cys Ser Ala Cys Gly Glu Thr Val Met Pro Gly Ser

                  100   105   110

Arg Lys Leu Glu Tyr Gly Gly Gln Thr Trp His Glu His Cys Phe Leu

        115   120   125

Cys Ile Gly Cys Glu Gln Pro Leu Gly Ser Arg Pro Phe Val Pro Asp

        130   135   140

5 Lys Gly Ala His Tyr Cys Val Pro Cys Tyr Glu Asn Asn Phe Ala Pro

       145   150   155   160

Arg Cys Ala Arg Cys Thr Lys Thr Leu Thr Gln Gly Gly Leu Thr Tyr

               165   170   175

Arg Asp Leu Pro Trp His Pro Lys Cys Leu Val Cys Thr Gly Cys Gln

10   180   185   190

Thr Pro Leu Ala Gly Gln Gln Phe Thr Ser Arg Asp Glu Asp Pro Tyr

               195   200   205

Cys Val Ala Cys Phe Gly Glu Leu Phe Ala Pro Lys Cys Ser Ser Cys

           210   215   220

15 Lys Arg Pro Ile Val Gly Leu Gly Gly Gly Lys Tyr Val Ser Phe Glu

   225   230   235   240

Asp Arg His Trp His His Asn Cys Phe Thr Cys Asp Arg Cys Ser Asn

               245   250   255

Ser Leu Val Gly Gln Gly Phe Val Pro Asp Gly Asp Gln Val Leu Cys

20   260   265   270

Gln Gly Cys Ser Gln Ala Gly Pro

       275   280

<210>   107

<211>   133

<212>   PRT

<213>   Homo sapiens

5   <220>

<221>   Cytochrome b5

<222>   (1)..(133)

<223>   Accession No. as of 29 August 2003: P00167

<400>   107

10

Ala Glu Gln Ser Asp Glu Ala Val Lys Tyr Tyr Thr Leu Glu Glu Ile

1   5   10   15

Gln Lys His Asn His Ser Lys Ser Thr Trp Leu Ile Leu His His Lys

              20   25   30

15 Val Tyr Asp Leu Thr Lys Phe Leu Glu Glu His Pro Gly Gly Glu Glu

              35   40   45

Val Leu Arg Glu Gln Ala Gly Gly Asp Ala Thr Glu Asn Phe Glu Asp

              50   55   60

Val Gly His Ser Thr Asp Ala Arg Glu Met Ser Lys Thr Phe Ile Ile

20 65   70   75   80

Gly Glu Leu His Pro Asp Asp Arg Pro Lys Leu Asn Lys Pro Pro Glu

              85   90   95

Thr Leu Ile Thr Thr Ile Asp Ser Ser Ser Ser Trp Trp Thr Asn Trp

              100   105   110

Val Ile Pro Ala Ile Ser Ala Val Ala Val Ala Leu Met Tyr Arg Leu

        115   120   125

Tyr Met Ala Glu Asp

        130

5

<210>   108

<211>   175

<212>   PRT

10 <213>   Homo sapiens

<220>

<221>   Pancreatitis-associated protein 1 precursor

<222>   (1)..(175)

<223>   Accession No. as of 29 August 2003: Q06141

15 <400>   108

Met Leu Pro Pro Met Ala Leu Pro Ser Val Ser Trp Met Leu Leu Ser

1   5   10   15

Cys Leu Met Leu Leu Ser Gln Val Gln Gly Glu Glu Pro Gln Arg Glu

20   20   25   30

Leu Pro Ser Ala Arg Ile Arg Cys Pro Lys Gly Ser Lys Ala Tyr Gly

        35   40   45

Ser His Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser Trp Thr Asp Ala

        50   55   60

Asp Leu Ala Cys Gln Lys Arg Pro Ser Gly Asn Leu Val Ser Val Leu

65   70   75   80

Ser Gly Ala Glu Gly Ser Phe Val Ser Ser Leu Val Lys Ser Ile Gly

                    85   90   95

5   Asn Ser Tyr Ser Tyr Val Trp Ile Gly Leu His Asp Pro Thr Gln Gly

                100   105   110

Thr Glu Pro Asn Gly Glu Gly Trp Glu Trp Ser Ser Ser Asp Val Met

                115   120   125

Asn Tyr Phe Ala Trp Glu Arg Asn Pro Ser Thr Ile Ser Ser Pro Gly

10   130   135   140

His Cys Ala Ser Leu Ser Arg Ser Thr Ala Phe Leu Arg Trp Lys Asp

145   150   155   160

Tyr Asn Cys Asn Val Arg Leu Pro Tyr Val Cys Lys Phe Thr Asp

                165   170   175

15

<210> 109

<211> 1028

<212> PRT

20 <213> Homo sapiens

<220>

<221> Collagen alpha 1(VI) chain precursor

<222> (1)..(1028)

<223> Accession No. as of 29 August 2003: P12109

<400> 109

```
        Met Arg Ala Ala Arg Ala Leu Leu Pro Leu Leu Leu Gln Ala Cys Trp
        1               5                   10                  15

   5    Thr Ala Ala Gln Asp Glu Pro Glu Thr Pro Arg Ala Val Ala Phe Gln
                        20                  25                  30

        Asp Cys Pro Val Asp Leu Phe Phe Val Leu Asp Thr Ser Glu Ser Val
                        35                  40                  45

        Ala Leu Arg Leu Lys Pro Tyr Gly Ala Leu Val Asp Lys Val Lys Ser
  10        50                  55                  60

        Phe Thr Lys Arg Phe Ile Asp Asn Leu Arg Asp Arg Tyr Tyr Arg Cys
        65                  70                  75                  80

        Asp Arg Asn Leu Val Trp Asn Ala Gly Ala Leu His Tyr Ser Asp Glu
                        85                  90                  95

  15    Val Glu Ile Ile Gln Gly Leu Thr Arg Met Pro Gly Gly Arg Asp Ala
                        100                 105                 110

        Leu Lys Ser Ser Val Asp Ala Val Lys Tyr Phe Gly Lys Gly Thr Tyr
                        115                 120                 125

        Thr Asp Cys Ala Ile Lys Lys Gly Leu Glu Gln Leu Leu Val Gly Gly
  20        130                 135                 140

        Ser His Leu Lys Glu Asn Lys Tyr Leu Ile Val Val Thr Asp Gly His
        145                 150                 155                 160

        Pro Leu Glu Gly Tyr Lys Glu Pro Cys Gly Gly Leu Glu Asp Ala Val
                        165                 170                 175
```

Asn Glu Ala Lys His Leu Gly Val Lys Val Phe Ser Val Ala Ile Thr
        180   185   190

Pro Asp His Leu Glu Pro Arg Leu Ser Ile Ile Ala Thr Asp His Thr
        195   200   205

5   Tyr Arg Arg Asn Phe Thr Ala Ala Asp Trp Gly Gln Ser Arg Asp Ala
        210   215   220

Glu Glu Ala Ile Ser Gln Thr Ile Asp Thr Ile Val Asp Met Ile Lys
225   230   235   240

Asn Asn Val Glu Gln Val Cys Cys Ser Phe Glu Cys Gln Pro Ala Arg
10   245   250   255

Gly Pro Pro Gly Leu Arg Gly Asp Pro Gly Phe Glu Gly Glu Arg Gly
            260   265   270

Lys Pro Gly Leu Pro Gly Glu Lys Gly Glu Ala Gly Asp Pro Gly Arg
            275   280   285

15 Pro Gly Asp Leu Gly Pro Val Gly Tyr Gln Gly Met Lys Gly Glu Lys
        290   295   300

Gly Ser Arg Gly Glu Lys Gly Ser Arg Gly Pro Lys Gly Tyr Lys Gly
305   310   315   320

Glu Lys Gly Lys Arg Gly Ile Asp Gly Val Asp Gly Val Lys Gly Glu
20   325   330   335

Met Gly Tyr Pro Gly Leu Pro Gly Cys Lys Gly Ser Pro Gly Phe Asp
        340   345   350

Gly Ile Gln Gly Pro Pro Gly Pro Lys Gly Asp Pro Gly Ala Phe Gly
        355   360   365

Leu Lys Gly Glu Lys Gly Glu Pro Gly Ala Asp Gly Glu Ala Gly Arg

     370   375   380

Pro Gly Ala Arg Gly Pro Ser Gly Asp Glu Gly Pro Ala Gly Glu Pro

     385   390   395   400

5 Gly Pro Pro Gly Glu Lys Gly Glu Ala Gly Asp Glu Gly Asn Pro Gly

           405   —   410   415

Pro Asp Gly Ala Pro Gly Glu Arg Gly Gly Pro Gly Glu Arg Gly Pro

       420   425   430

Arg Gly Thr Pro Gly Pro Arg Gly Pro Arg Gly Asp Pro Gly Glu Ala

10   435   440   445

Gly Pro Gln Gly Asp Gln Gly Arg Glu Gly Pro Val Gly Val Pro Gly

      450   455   460

Asp Pro Gly Glu Ala Gly Pro Ile Gly Pro Lys Gly Tyr Arg Gly Asp

     465   470   475   480

15 Glu Gly Pro Pro Gly Ser Glu Gly Ala Arg Gly Ala Pro Gly Pro Ala

             485   490   495

Gly Pro Pro Gly Asp Pro Gly Leu Met Gly Glu Arg Gly Glu Asp Gly

       500   505   510

Pro Ala Gly Asn Gly Thr Glu Gly Phe Pro Gly Phe Pro Gly Tyr Pro

20   515   520   525

Gly Asn Arg Gly Ala Pro Gly Ile Asn Gly Thr Lys Gly Tyr Pro Gly

      530   535   540

Leu Lys Gly Asp Glu Gly Glu Ala Gly Asp Pro Gly Asp Asp Asn Asn

545   550   555   560

Asp Ile Ala Pro Arg Gly Val Lys Gly Ala Lys Gly Tyr Arg Gly Pro
565   570   575

Glu Gly Pro Gln Gly Pro Pro Gly His Gln Gly Pro Pro Gly Pro Asp
580   585   590

5   Glu Cys Glu Ile Leu Asp Ile Ile Met Lys Met Cys Ser Cys Cys Glu
595   600   605

Cys Lys Cys Gly Pro Ile Asp Leu Leu Phe Val Leu Asp Ser Ser Glu
610   615   620

Ser Ile Gly Leu Gln Asn Phe Glu Ile Ala Lys Asp Phe Val Val Lys
10 625   630   635   640

Val Ile Asp Arg Leu Ser Arg Asp Glu Leu Val Lys Phe Glu Pro Gly
645   650   655

Gln Ser Tyr Ala Gly Val Val Gln Tyr Ser His Ser Gln Met Gln Glu
660   665   670

15 His Val Ser Leu Arg Ser Pro Ser Ile Arg Asn Val Gln Glu Leu Lys
675   680   685

Glu Ala Ile Lys Ser Leu Gln Trp Met Ala Gly Gly Thr Phe Thr Gly
690   695   700

Glu Ala Leu Gln Tyr Thr Arg Asp Gln Leu Leu Pro Pro Ser Pro Asn
20 705   710   715   720

Asn Arg Ile Ala Leu Val Ile Thr Asp Gly Arg Ser Asp Thr Gln Arg
725   730   735

Asp Thr Thr Pro Leu Asn Val Leu Cys Ser Pro Gly Ile Gln Val Val
740   745   750

Ser Val Gly Ile Lys Asp Val Phe Asp Phe Ile Pro Gly Ser Asp Gln

　　　　755　　　　　　　　　760　　　　　　　　765

Leu Asn Val Ile Ser Cys Gln Gly Leu Ala Pro Ser Gln Gly Arg Pro

　　　　770　　　　　　　　　775　　　　　　　　780

5　Gly Leu Ser Leu Val Lys Glu Asn Tyr Ala Glu Leu Leu Glu Asp Ala

　　　785　　　　　　　　790　　　　　　　　795　　　　　　　800

Phe Leu Lys Asn Val Thr Ala Gln Ile Cys Ile Asp Lys Lys Cys Pro

　　　　　　　805　　　　　　　　810　　　　　　　815

Asp Tyr Thr Cys Pro Ile Thr Phe Ser Ser Pro Ala Asp Ile Thr Ile

10　　　　　820　　　　　　　　825　　　　　　　　830

Leu Leu Asp Gly Ser Ala Ser Val Gly Ser His Asn Phe Asp Thr Thr

　　　　835　　　　　　　　840　　　　　　　　845

Lys Arg Phe Ala Lys Arg Leu Ala Glu Arg Phe Leu Thr Ala Gly Arg

　　　850　　　　　　　855　　　　　　　860

15　Thr Asp Pro Ala His Asp Val Arg Val Ala Val Val Gln Tyr Ser Gly

　865　　　　　　　　870　　　　　　　875　　　　　　　880

Thr Gly Gln Gln Arg Pro Glu Arg Ala Ser Leu Gln Phe Leu Gln Asn

　　　　　　　885　　　　　　　890　　　　　　　895

Tyr Thr Ala Leu Ala Ser Ala Val Asp Ala Met Asp Phe Ile Asn Asp

20　　　　900　　　　　　　905　　　　　　　910

Ala Thr Asp Val Asn Asp Ala Leu Gly Tyr Val Thr Arg Phe Tyr Arg

　　　915　　　　　　　920　　　　　　　925

Glu Ala Ser Ser Gly Ala Ala Lys Lys Arg Leu Leu Leu Phe Ser Asp

　　　930　　　　　　　935　　　　　　　940

Gly Asn Ser Gln Gly Ala Thr Pro Ala Ala Ile Glu Lys Ala Val Gln

945　　　　　　　950　　　　　　　955　　　　　　　960

Glu Ala Gln Arg Ala Gly Ile Glu Ile Phe Val Val Val Val Gly Arg

965　　　　　　　970　　　　　　　975

5　Gln Val Asn Glu Pro His Ile Arg Val Leu Val Thr Gly Lys Thr Ala

980　　　　　　　985　　　　　　　990

Glu Tyr Asp Val Pro Tyr Gly Glu Ser His Leu Phe Arg Val Pro Ser

995　　　　　　　1000　　　　　　　1005

Tyr Gln Ala Leu Leu Arg Gly Val Phe His Gln Thr Val Ser Arg

10　　1010　　　　　　　1015　　　　　　　1020

Lys Val Ala Leu Gly

1025

15　<210>　110

<211>　338

<212>　PRT

<213>　Homo sapiens

<220>

20　<221>　Lumican precursor

<222>　(1)..(338)

<223>　Accession No. as of 29 August 2003: P51884

<400>　110

Met Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr

1   5   10   15

Ser Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln

                20   25   30

5   Ser Ser Pro Asn Cys Ala Pro Glu Cys Asn Cys Pro Glu Ser Tyr Pro

                35   40   45

Ser Ala Met Tyr Cys Asp Glu Leu Lys Leu Lys Ser Val Pro Met Val

        50   55   60

Pro Pro Gly Ile Lys Tyr Leu Tyr Leu Arg Asn Asn Gln Ile Asp His

10 65   70   75   80

Ile Asp Glu Lys Ala Phe Glu Asn Val Thr Asp Leu Gln Trp Leu Ile

                85   90   95

Leu Asp His Asn Leu Leu Glu Asn Ser Lys Ile Lys Gly Arg Val Phe

                100   105   110

15 Ser Lys Leu Lys Gln Leu Lys Lys Leu His Ile Asn His Asn Asn Leu

            115   120   125

Thr Glu Ser Val Gly Pro Leu Pro Lys Ser Leu Glu Asp Leu Gln Leu

            130   135   140

Thr His Asn Lys Ile Thr Lys Leu Gly Ser Phe Glu Gly Leu Val Asn

20 145   150   155   160

Leu Thr Phe Ile His Leu Gln His Asn Arg Leu Lys Glu Asp Ala Val

                165   170   175

Ser Ala Ala Phe Lys Gly Leu Lys Ser Leu Glu Tyr Leu Asp Leu Ser

                180   185   190

Phe Asn Gln Ile Ala Arg Leu Pro Ser Gly Leu Pro Val Ser Leu Leu
          195   200   205

Thr Leu Tyr Leu Asp Asn Asn Lys Ile Ser Asn Ile Pro Asp Glu Tyr
          210   215   220

5 Phe Lys Arg Phe Asn Ala Leu Gln Tyr Leu Arg Leu Ser His Asn Glu
   225   230   235   240

Leu Ala Asp Ser Gly Ile Pro Gly Asn Ser Phe Asn Val Ser Ser Leu
              245   250   255

Val Glu Leu Asp Leu Ser Tyr Asn Lys Leu Lys Asn Ile Pro Thr Val
10   260   265   270

Asn Glu Asn Leu Glu Asn Tyr Tyr Leu Glu Val Asn Gln Leu Glu Lys
              275   280   285

Phe Asp Ile Lys Ser Phe Cys Lys Ile Leu Gly Pro Leu Ser Tyr Ser
          290   295   300

15 Lys Ile Lys His Leu Arg Leu Asp Gly Asn Arg Ile Ser Glu Thr Ser
   305   310   315   320

Leu Pro Pro Asp Met Tyr Glu Cys Leu Arg Val Ala Asn Glu Val Thr
              325   330   335

Leu Asn

20